

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 00:01:33 ; Search time 4609 Seconds  
(without alignments)  
2153.516 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Fgapext 7.0  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1258	100.0	1106	6	AX016287 Sequence
2	1258	100.0	1106	6	BD137019 Human CAS
3	1258	100.0	1158	6	AX016289 Sequence
4	1258	100.0	1158	6	BD137020 Human CAS
5	1258	100.0	1181	9	AB013730 Homo sapi
6	1258	100.0	1186	9	AB012917 Homo sapi
7	1258	100.0	1192	6	AR152174 Sequence
8	1258	100.0	1204	6	AX358932 Sequence
9	1258	100.0	1204	6	AX362425 Sequence
10	1258	100.0	1204	6	AX454622 Sequence
11	1258	100.0	1204	6	AX464372 Sequence
12	1258	100.0	1204	6	AX491100 Sequence
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15	1258	100.0	1213	9	BC022068 Homo sapi
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ALIGNMENTS

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LOCUS AX016287 1106 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1 from Patent WO9949055.  
ACCESSION AX016287  
VERSION AX016287.1 GI:10041854  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P., and Vinals-Bassols,C.  
TITLE Human casb12 polypeptide, a serine protease  
JOURNAL Patent: WO 9949055-A 1 30-SEP-1999;  
SMITHKLINE BEECHAM BIOLOG (BE);  
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA (BE)  
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DB 293 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGCGAGCACAACCTCCAGAGGAGGAG 352  
QY 61 GlyCysGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80  
DB 353 GGCTGTGAGCAGACCCGAGCAGCACTGAGTCTCTCCCGCCCGGCTTCAACACAGC 412  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 413 CTCCCCAACAAGACCAACCGCATGATCATCTGCTGAGATGATGATGATGATGATGATGAT 472  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 473 ATCACTGGGCTGTGGAGCCCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 532  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
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DEFINITION Human CASB 12 polypeptide, a serine protease.  
ACCESSION BD137019  
VERSION BD137019.1 GI:23231964  
KEYWORDS JP12002507425-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.  
TITLE Human CASB 12 polypeptide, a serine protease  
JOURNAL Patent: JP 2002507425-A 1 12-MAR-2002;  
SMITHKLINE BEECHAM BIOLOGICALS SA  
COMMENT OS Homo sapiens (human)  
PN JP 2002507425-A/1  
PD 12-MAR-2002  
PF 17-MAR-1999 JP 2000538015  
PR 20-MAR-1998 GB 9806095.7  
PI CLAUDINE ELVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI CARLOTA VINALS BASSOLS  
PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,  
PC C12N1/15,  
PC C12N1/19,C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12Q1/02,C12Q1/  
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Best Local Similarity: 100.00% Mismatches: 0  
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QY 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThraAla 40  
DB 233 AAGACGGGGTACTCTGTGGGGGAGCGCTCATGCCGCCAGATGGTCTCTGACGAGCC 292  
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnysGlu 60  
DB 293 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGCGAGCACAACCTCCAGAGGAGGAG 352  
QY 61 GlyCysGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80

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Qy     121  CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db      533  TGCCTCATTTCCGGCTGGGCGACGACGCTCCAGCCGCCCACTTACGGCTGCTCACACCTTG 592
Qy     141  ArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db      593  CGATGGCCCAACATCACCATCATTTGAGCACCAAGAGTGTGAAGCGCTTACCCCGGCAAC 652
Qy     161  IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180
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Qy     181  AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
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Qy     201  AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db      773  GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAATATGTGGAC 832
Qy     221  TrpIleGlnGluThrMetLysAsnAsn 229
Db      833  TGGATCCAGGACGATGAAGAACAT 859

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LOCUS      AX016289                1158 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent WO9949055.
ACCESSION AX016289
VERSION    AX016289.1 GI:10041855
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE      Human casb12 polypeptide, a serine protease
JOURNAL    Patent: WO 9949055-A 3 30-SEP-1999; SMITHKLINE BEECHAM BIOLOG (BE);
           BRUCK CLAUDEINE ELVIRE MARIE (BE); VINALS BASSOLS CARLOTA
           COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
           (BE)

FEATURES   Location/Qualifiers
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Qy     61  GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
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Qy     81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
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Qy    101  IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
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Qy    121  CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
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Qy    141  ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
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Qy    161  IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180
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Db     843  GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAATATGTGGAC 902
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LOCUS      BD137020                1158 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Human CASB 12 polypeptide, a serine protease.
ACCESSION BD137020
VERSION    BD137020.1 GI:23231965
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
TITLE      Human CASB 12 polypeptide, a serine protease
JOURNAL    Patent: JP 2002507425-A 2 12-MAR-2002;
           SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT     OS Homo sapiens (human)
            PN JP 2002507425-A/2
            PD 12-MAR-2002
            PF 17-MAR-1999 JP 2000538015
            PR 20-MAR-1998 GB 9806095.7
            PI CLAUDEINE ELVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI
            CARLOTA VINALS BASSOLS
            PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,
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Db 604 CGATGCCCCACATCATTCATTTGAGCACAGAGGTGAGAACGCTACCCCGGCAAC 663

Qy 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180

Db 664 ATCAGACACCATGGTGTGTGCAGCGTGCAGGAGGGGCGAGGACTCTCTCCAGGGT 723

Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200

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Qy 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysValValAsp 220

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LOCUS

DEFINITION Homo sapiens mRNA for serine protease (TLSP), complete cds.

ACCESSION AB012917

VERSION AB012917.1 GI:3649790

KEYWORDS TLSP; serine protease (TLSP).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

Yoshida S., Taniguchi M., Suemoto T., Oka T., He X. and Shiozaka S. cDNA cloning and expression of a novel serine protease, TLSP Blochim. Biophys. Acta 1399 (2-3), 225-228 (1998)

98438738

7975601

REFERENCE 2 (bases 1 to 1186)

Yoshida S.

Direct Submission

Submitted (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1, Asahikawa Medical College, Midorigaoka Higashi 2-1-1, Asahikawa, Hokkaido 078-8510, Japan (E-mail: syoshida@asahikawa-med.ac.jp, Tel: 81-166-68-2300, Fax: 81-166-68-2309)

Location/Qualifiers

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polyA\_signal 1164. .1169

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/note="12 a nucleotides"

ORIGIN

Alignment Scores:

Pred. No.: 4, 85e-97 Length: 1186

Score: 1258.00 Matches: 229

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

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Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThAlaAla 40

Db 245 AAGACGGCGTACTCTGTGGGGCGACGCTCATCGCCCCAGATGGCTCTCGACAGCACC 304

Qy 41 HisCysLeuLysProArgTrpIleValHisGlnGlnHisAsnLeuGlnLysGluGlu 60

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Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80

Db 365 GGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTTCCCCACCCTCCGCTTCAACAACAGC 424

Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100

Db 425 CTCGCCCAACAGACCCAGCAATGACATCATGTGTGAAGATGGCATCGCCAGTCTCC 484

Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120

Db 485 ATCACCCTGGGCTGTGGACCCCTCACCTCTCTCACGCTGTGTCTGTGGACCCAGC 544

Qy 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140

Db 545 TGCCTCATTTCCGCTGGGCGAGCAGCTCCAGCCCGCCAGTTACGCTCTCCCTCACACCTTG 604

Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160

Db 605 CGATCGGCGCAACATCACCATCATTTGAGCACCAGAGGTGTGAGAACGCTACCCCGGCAAC 664

Qy 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180

Db 665 ATCAGACACCATGGTGTGTGGCGAGCAGCTCCAGCCCGCCAGTTACGCTCTCCCTCACACCTTG 724

Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200

Db 725 GACTCCGGGGGCGCTCTGTGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTCGGGCCAG 784

Qy 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysValValAsp 220

Db 785 GATCCGTGTGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAC 844

Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229

Db 845 TGGATCCAGGAGACGATGAAGACAAT 871

RESULT 7

AB012917

LOCUS

DEFINITION Sequence 8 from patent US 6232456.

ACCESSION AB012917

VERSION AB012917.1 GI:15118224

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1192)

Cohen M., Colpitts T.L., Friedman P.N., Granados E., Klass M.R., Russell J.C., Stewart K.D. and Stroupe S.D. Serine protease reagents and methods useful for detecting and

JOURNAL  
 FEATURES  
 source  
 treating diseases of the prostate  
 Patent: US 6232456-A 8 15-MAY-2001;  
 Location/Qualifiers  
 1. 1192  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.88e-97 Length: 1192  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AR152174 (1-1192)

Qy 1 IlelelysglypheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
 Db 170 ATCATCAAGGGGTTTCGAGTGCAGGCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCGAG 229  
 Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
 Db 230 AAGACGGCGCTACTCTGTGGGGGACGCTCATGCCGCCAGATGGCTCTCCAGCAGGACC 289  
 Qy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
 Db 290 CACTGCCTCAAGCCCGCTACATAGTTCACTGGGGCAGCACAACTCCAGAGGAGGAG 349  
 Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
 Db 350 GGCTGTGAGCAGACCCCGACGACCTGAGTCTCTCCGCCACCCCGCTTCAACAACAGC 409  
 Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 410 CTCCCCCAACAAGACCCACCCGATGACATCATGCTGTGAGATGGCATGCCAGTCTCC 469  
 Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 470 ATCACTGGGCTGTGGACCCCTCACCTCTCTCTCAAGCTGTCTCACTGTGGCACCAGC 529  
 Qy 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 530 TGCCTCATTTCCGGCTGGGAGCAGCATCTCAGCCCCAGTTACGCTGCCTCACACTTG 589  
 Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaValProGlyAsn 160  
 Db 590 CGATGCGCAACATCAACCATTCATTGACACAGAGTGTGAGAACGCTTACCCCGGCAAC 649  
 Qy 161 IleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGly 180  
 Db 650 ATCAGACACACCATGGTGTGGCAGCGTGCAGAGGGGGGAGGACTCTCCGCAAGGT 709  
 Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 710 GACTCCGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTGGGGCCAG 769  
 Qy 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 220  
 Db 770 GATCCGTGTGGATCACCCGAAAGCCCTGGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 829  
 Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229  
 Db 830 TGGATCCAGGAGACGATGAAGAACAAT 856

RESULT 8  
 AX358932  
 LOCUS  
 DEFINITION Sequence 185 from Patent WO0193983.  
 ACCESSION AX358932  
 VERSION AX358932.1 GI:18675367  
 KEYWORDS  
 linear PAT 13-FEB-2002

## SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Goddard, J.P.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same

JOURNAL Patent: WO 0193983-A 185 13-DEC-2001;  
 Genentech Inc. (US)

## FEATURES

source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.93e-97 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AX358932 (1-1204)

Qy 1 IlelelysglypheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
 Db 169 ATCATCAAGGGGTTTCGAGTGCAGGCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCGAG 228  
 Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
 Db 229 AAGACGGCGCTACTCTGTGGGGGACGCTCATGCCGCCAGATGGCTCTCCAGCAGGACC 288  
 Qy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
 Db 289 CACTGCCTCAAGCCCGCTACATAGTTCACTGGGGCAGCACAACTCCAGAGGAGGAG 348  
 Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
 Db 349 GGCTGTGAGCAGACCCCGACGACCTGAGTCTCTCCGCCACCCCGCTTCAACAACAGC 408  
 Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 409 CTCCCCCAACAAGACCCACCCGATGACATCATGCTGTGAGATGGCATGCCAGTCTCC 468  
 Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 469 ATCACTGGGCTGTGGACCCCTCACCTCTCTCTCAAGCTGTCTCACTGTGGCACCAGC 528  
 Qy 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 529 TGCCTCATTTCCGGCTGGGAGCAGCATCTCAGCCCCAGTTACGCTGCCTCACACTTG 588  
 Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaValProGlyAsn 160  
 Db 589 CGATGCGCAACATCAACCATTCATTGACACAGAGTGTGAGAACGCTTACCCCGGCAAC 648  
 Qy 161 IleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGly 180  
 Db 649 ATCAGACACACCATGGTGTGGCAGCGTGCAGAGGGGGGAGGACTCTCCGCAAGGT 708  
 Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTGGGGCCAG 768  
 Qy 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 220  
 Db 769 GATCCGTGTGGATCACCCGAAAGCCCTGGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 828

QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
 Db 829 TGGATCCAGGAGACGATGAAGACAAT 855

RESULT 9  
 AX362425 1204 bp DNA linear PAT 15-FEB-2002  
 LOCUS  
 DEFINITION Sequence 185 from Patent WO0208288.  
 ACCESSION AX362425  
 VERSION AX362425.1 GI:18694670  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0208288-A 185 31-JAN-2002;  
 Genentech, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

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 Pred. No.: 1258.00 Matches: 229  
 Score: 1258.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AX362425 (1-1204)

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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40  
 Db 229 AAGACGGGCTACTCTGTGGGGGAGCTCATCGCCCCCAGATGGCTCTGTGACAGGCC 288

QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
 Db 289 CACTGTGCTCAAGCCCGCTACATAGTTACCTGGGGCAGCAACCTCCAGAAGGAGGAG 348

QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
 Db 349 GGCTGTGAGCAGACCCGGAGCCACTGAGTCTCTTCCCCACCCCGGCTTCAACACAGC 408

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 409 CTCCCCAACAAAGACACCGCAATGACATCATGCTGGTGAAGATGGCATGGCAGTCTCC 468

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 469 ATCACTGGGGCTGTGCGACCCCTCCCTCCCTCCTCAGCTGTGTCACTGCTGGCCACAGC 528

QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCCCAGTTACGCTGCTCCTACACCTTG 588

QY 141 ArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsnAlaTrpProGlyAsn 160  
 Db 589 CGATGGCCCAACATCACCATCATTTGAGCACCAGAGAGTGTGAGACGCTACCCCGGCAAC 648

QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180

Db 649 ATCAGACACCATGGTGTGTGCCAGCGTCAGGAAGGGGCAAGGACTCTCTGCCAGGGT 708

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGGCGCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTCTGGGGCCAG 768

QY 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220  
 Db 769 GATCGGTGTGCGATCACCCGAAAGCCTGTGTACACGAAAGTCTGCAAAATATGTGAC 828

QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
 Db 829 TGGATCCAGGAGACGATGAAGACAAT 855

RESULT 10  
 AX454622 1204 bp DNA linear PAT 06-JUL-2002  
 LOCUS  
 DEFINITION Sequence 207 from Patent WO0208284.  
 ACCESSION AX454622  
 VERSION AX454622.1 GI:21713935  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.  
 TITLE Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 JOURNAL Patent: WO 0208284-A 207 31-JAN-2002;  
 Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone  
 (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,  
 Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);  
 Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);  
 Paoni, Nicholas F. (US); Marsters, Scot A. (US); Stephan, Jean-Philippe F. (US);  
 Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William  
 I. (US)

FEATURES  
 source Location/Qualifiers  
 1..1204  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Alignment Scores: 4.93e-97 Length: 1204  
 Pred. No.: 1258.00 Matches: 229  
 Score: 1258.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AX454622 (1-1204)

QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
 Db 169 ATCATCAAGGGTTCAGTGCAGGCTCATCTCCAGCCCTGGCAGCCCTGTTTCGAG 228

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40  
 Db 229 AAGACGGGCTACTCTGTGGGGGAGCTCATCGCCCCCAGATGGCTCTGTGACAGGCC 288

QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
 Db 289 CACTGTGCTCAAGCCCGCTACATAGTTACCTGGGGCAGCAACCTCCAGAAGGAGGAG 348

QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
 Db 349 GGCTGTGAGCAGACCCGGAGCCACTGAGTCTCTTCCCCACCCCGGCTTCAACACAGC 408

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 409 CTCCCCAACAAAGACACCGCAATGACATCATGCTGGTGAAGATGGCATGGCAGTCTCC 468

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 469 ATCACTGGGGCTGTGCGACCCCTCCCTCCCTCCTCAGCTGTGTCACTGCTGGCCACAGC 528

QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCCCAGTTACGCTGCTCCTACACCTTG 588

QY 141 ArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsnAlaTrpProGlyAsn 160  
 Db 589 CGATGGCCCAACATCACCATCATTTGAGCACCAGAGAGTGTGAGACGCTACCCCGGCAAC 648

QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180

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QY      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db      409 CTCCCAACAAAGACCAACCGCATGACATCATGCTGCTGAGATGGCATCGCCAGTCTCC 468

QY      101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db      469 ATCACCTGGCTGCTGGCGACCCCTCACCTCTCTCTACCGCTGTGTCACTCTGCGCACCG 528

QY      121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db      529 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTAGCTGCTCTCACCTTGG 588

QY      141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160
Db      589 CGATGGCCCAACATCACCATCATTTAGCACCAGACAGAGTGTGAGAACGCTTACCCCGCAAC 648

QY      161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCysGlnGly 180
Db      649 ATCACAGACACCATGCTGTGTGCGACGTCAGAGAGGGGGCAGGACCTCTGCGCAGGCT 708

QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleSerTrpGlyGln 200
Db      709 GATTCGGGGGGCCCTCTGGTCTGTACCATGCTCTTCAAGGCATTTATCTCTGGGGCCAG 768

QY      201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220
Db      769 GATCCGTTGTCGATCACCCGAAAGCCCTGTGTCTACACGAAAGTCTGCAATATGTGGAC 828

QY      221 TrpIleGlnGluThrMetLysAsnAsn 229
Db      829 TGGATCCAGGAGAGATGAAGAACAAAT 855

RESULT 11
AX464372 1204 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 505 from Patent WO0140466.
ACCESSION AX464372
VERSION AX464372.1 GI:21899202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tamas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 505 07-JUN-2001;
Genentech Inc. (US)
FEATURES
source Location/Qualifiers
1..1204
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 4.93e-97 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x AX464372 (1-1204)

QY      1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
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QY      21  LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
Db      229 AAGACGGGGTACTCTGTGGGGGACGCTCATCGCCCCAGATGGCTCTGTGACAGAGCC 288

QY      41  HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db      289 CACTGCTCTAAGCCCGCTACATAGTTCACTTGGGGCAGCACAACCTCCAGAGAGGGAG 348

QY      61  GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db      349 GGCTGTGAGCAGACCCGACAGCCAGCTAGTCTTTCCTCCACCCCGGCTTCAACAACAGC 408

QY      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db      409 CTCCCAACAAAGACCAACCGCATGACATCATGCTGCTGAGATGGCATCGCCAGTCTCC 468

QY      101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db      469 ATCACCTGGCTGCTGGCGACCCCTCACCTCTCTCTACCGCTGTGTCACTCTGCGCACCG 528

QY      121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db      529 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTAGCTGCTCTCACCTTGG 588

QY      141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160
Db      589 CGATGGCCCAACATCACCATCATTTAGCACCAGACAGAGTGTGAGAACGCTTACCCCGCAAC 648

QY      161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCysGlnGly 180
Db      649 ATCACAGACACCATGCTGTGTGCGACGTCAGAGAGGGGGCAGGACCTCTGCGCAGGCT 708

QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleSerTrpGlyGln 200
Db      709 GATTCGGGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTTATCTCTGGGGCCAG 768

QY      201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220
Db      769 GATCCGTTGTCGATCACCCGAAAGCCCTGTGTCTACACGAAAGTCTGCAATATGTGGAC 828

QY      221 TrpIleGlnGluThrMetLysAsnAsn 229
Db      829 TGGATCCAGGAGAGATGAAGAACAAAT 855

RESULT 12
AX491100 1204 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 207 from Patent WO0200690.
ACCESSION AX491100
VERSION AX491100.1 GI:22323887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 207 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:

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Pred. No.: 4.93e-97 Length: 1204  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AX491100 (1-1204)

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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40  
Db 229 AGACGGGGTACTCTGTGGGGCAGCGCTCATCGCCCCAGATGGCTCTCTGACAGCAGCC 288

QY 41 HisCysLeuIysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
Db 289 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGCAGCAGCAACCTCCAGAGGAGGAG 348

QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 349 GGCTGTGAGCAGACCCGAGCCACTGAGTCTCTCCCAACCCCGGCTTCAACACAGC 408

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 409 CTCCCCAACAAAGACCAACCGCAATGACATCATGTGTGAAGATGGCATCGCCAGTCTCC 468

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
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LOCUS  
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AX697101  
VERSION  
AX697101.1 GI:29498066  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS  
Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.

TITLE  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL  
Patent: WO 0078961-A 169 28-DEC-2000;  
Genentech Inc. (US)  
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Location/Qualifiers  
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US-09-856-320A-2\_COPY\_54\_282 (1-229) x AX697101 (1-1204)

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QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
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QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
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RESULT 14  
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LOCUS  
DEFINITION  
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## JOURNAL

Submitted (22-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk

Email: [cgabs-i@mail.nih.gov](mailto:cgabs-i@mail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: [amadane@systemsbiology.org](mailto:amadane@systemsbiology.org)

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 46 Row: m Column: 6  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21618355.

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193..861

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/db\_xref="CDD:smart00020"

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-09-856-320A-2\_COPY\_54\_282 (1-229) x BC022068 (1-1213)

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QY	41	HisCysLeuLysProArgTrrleValHisLeuGlyGlnHisAsnLeuGlnLysGlu	60

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Db	616	CGATGCGCCAAACATCACCCTCATTTGAGCACCAGAGTGTGAGAACGCTACCCCGGCAAC	675
QY	161	IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly	180
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Search completed: June 23, 2004, 03:02:09

Job time : 4617 secs

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; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-944-483-8
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; Alignment Scores:
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; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
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; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-189

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; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0481 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNG TUIT10
; CLONE: 2723646
US-09-025-059-2

Alignment Scores:
Pred. No.:      8,49e-125      Length:      1314
Score:          1258.00      Matches:      229
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              3      Gaps:      0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-025-059-2 (1-1314)

QY      1      IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
DB      287      ATCATCAAGGGTTCAGTGTGAGTGTCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTCTTCGAG 346
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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
Db 347 AAGAGCGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGGCTCTGACAGCGCC 406  
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
Db 407 CACTGCCTCAAGCCCGCTACATAGTTCACTCGGGGAGCAGCACTCCAGAGGAGGAG 466  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 467 GGCTGTGAGCAGAGCCCGGAGCAGCAGTGTCTTCCCGCCAGCCCGGCTTCAACACAGC 526  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 527 CTCCCAACCAAGACCAACCGCAATGATCATCTGTGGAAGATGATGCGCAGTCTCC 586  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 587 ATCACTGGGCTGTGGGAGCCCTTCACTCTCTCTGCTGTGTCTCTGCTGTGACCAAGC 646  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
Db 647 TGCTCATTTCCGGCTGGGAGCAGCAGTCTCCAGCCCGCAGTTACGCTGCTGTGACCACTG 706  
QY 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpPocGlyAsn 160  
Db 707 CGATGCCCGCAACATCACTCATTTGAGCAGCAGAGTGTGAGAACCGCTTACCCCGCAAC 766  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyCysLysAspSerCysGlnGly 180  
Db 767 ATCACAGACACCATGTGTGTGTCAGCGTGCCAGGAGGGGCAAGACTCTTGCACAGGT 826  
QY 181 AspSerGlyCysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 827 GACTCCGGGGGCGCTCTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 886  
QY 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysValValAsp 220  
Db 887 GATCCGTGTGCGATCACCCGAAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 946  
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
Db 947 TGGATCCAGGAGCAGTGAAGAACAAT 973  
  
RESULT 4  
US-09-205-258-247  
; Sequence 247, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,373  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,875  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,374  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,917  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,949  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,883  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,897  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,898  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,962  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,963  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,877  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,878  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/070,923  
; EARLIER FILING DATE: 1997-12-18  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1227  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 247  
; LENGTH: 1146  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (20)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:

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; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-205-258-247

Alignment Scores:
Pred. No.:      8 07e-124      Length:      1146
Score:          1248.00      Matches:      227
Percent Similarity: 99.13%      Conservative: 0
Best Local Similarity: 99.13%      Mismatches: 2
Query Match:      99.21%      Indels:      0
DB:              4          Gaps:      0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-205-258-247 (1-1146)
QY 1 IleileLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 124 ATCATCAAGGGTTCAGGTGCAAGCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCGAG 183
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db 184 AAGACGGGTACTCTGTGGGGGAGCGCTCATCGCCCGCAGATGGTCTCTGACGAGCC 243
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 244 CACTGGCTCAAGCCCGCTACATAGTTCACTGGGGCAGCACACCTCCAGAGGAGGAG 303
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
Db 304 GGCTGTGAGCAGACCCGAGCAGCAGTGTCTTCCCCCACCCTGGCTTCAACACAGC 363
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 364 CTCCCAACAAGACCCAGCATATGATCATCTGTGTGAAGTGGCATCGCCAGCTCC 423
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 424 ATCACTGGGCTGTGGACCCCTCACCTCTCTCAAGCTGTGTCTCACTGTCGACAGC 483
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 484 TGYCTCATTTCCGGCTGGGGCAGMACGTCCAGCCCCAGTTACGCTGCTCACACTTG 543
QY 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160
Db 544 SGATGCCCAACATCAACATCAATTGAGCAGCAGAGTGTGAGAACGCTACCCCGCAAC 603
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluClyGlyLysAspSerCysGlnGly 180
Db 604 ATCACAGACCACTGGTGTGGCAGCGTGCAGAGGGGGCAAGGACTCTCTCCAGGGT 663
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200
Db 664 GACTCCGGGGCCCTCTGGTCTGTGATACAGCTCTTCAAGGCATTATCTCTGGGGCCAG 723
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 220
Db 724 GATCCGTGTGGCATCACCCGAAAGCCCTGGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 783
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 784 TGGATCCAGGAGACGATGAGAAACAAT 810

RESULT 5
US-08-944-483-7

; Sequence 7, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-944-483-7

Alignment Scores:
Pred. No.:      1 35e-123      Length:      1166
Score:          1246.00      Matches:      227
Percent Similarity: 99.13%      Conservative: 0
Best Local Similarity: 99.13%      Mismatches: 2
Query Match:      99.05%      Indels:      0
DB:              3          Gaps:      0

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-944-483-7 (1-1166)
QY 1 IleileLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db 226 AARACGGGCTACTCTGTGGGGCAGCTCATCGCCCGCAGATGGCTCTGACAGCAGCC 285
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 286 CACTGGCTCAAGCCCGCTACATAGTTCACTGGGGCAGCACACCTCCAGAGGAGGAG 345
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
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Db 346 GGCTGTGAGCAGACCCGACGACCTGAGTCTTCCCCCACCCTCCGCTTCAACACAGC 405
Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 406 CTCCCCAACAAAGACCCGCAATGACATCATGCTGTGAAGATGGCATCGCCAGTCTCC 465
Qy 101 IleThrTrpAlaValArgProLeuThrLysSerSerArgCysValThrAlaGlyThrSer 120
Db 466 ATCACTCTGGGTGTGGCAGCCCTCACCTCTCTCTCACTGTGTCTCACTGTGGCAGCAGC 525
Qy 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db 526 TGCTCTCAATTCGGCTGGGCGACGACGCTCCAGCCCCCAGTTACGCTGCTCACACTTG 585
Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaThrProGlyAsn 160
Db 586 CGATGCGCCCAACATCACTATGAGCAGCAGAGGTGTGAGAACGCTTACCCCGGCAAC 645
Qy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180
Db 646 ATCACAGACCATGTGTGTGCGCAGCTGTGAGAGGGGGGCAAGGACTCTCTCCAGGGT 705
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 706 GACTCCGGGGGCCCTCTGGTCTGTAACTGCTCTTCAAGGCATTTATCTCTGGGCGCAG 765
Qy 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysThrValAsp 220
Db 766 GATCCGGTGGGATCAACCCGAAAGCCTGGTGTCTACACGAAAGTGTGCAAAATATGTGGAC 825
Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 826 TGGATCCAGGAGACGATGAAGAACAA 852
RESULT 6
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCES: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10
Alignment Scores:
Pred. No.: 7,84e-121 Length: 1052
Score: 1219.50 Matches: 223
Percent Similarity: 98.26% Conservative: 3
Best Local Similarity: 96.96% Mismatches: 3
Query Match: 96.94% Indels: 1
DB: 4 Gaps: 1
US-09-856-320A-2_COPY_54_282 (1-229) x US-09-386-642-10 (1-1052)
Qy 1 IleIleLysGlyPheGluCys---LysProHisSerGlnProTrpGlnAlaLeuPhe 19
Db 166 ATGTTGGGGGCTCACTCACTGTCTAGAAAGCATCCAGCCCTGGCAGGACCCCTGTTTC 225
Qy 20 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 39
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Db 226 GGAAGAGCCGGCTACTCTGTGGGCGACGCTATCGCCCCCAGATGCTCTCTACAGCA 285
Qy 40 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 59
Db 286 GCCCACTCGCTCAAGCCCGCTACATAGTTTCACTGGGCGACGACCAACCTCCAGAGGAG 345
Qy 60 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 79
Db 346 GAGGGCTGTGAGCAGACCCGACGACCTGAGTCTTCCCTCCCTCCCTCCCTCCCTCCCT 405
Qy 80 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 99
Db 406 AGCTCTCCCAACAAAGACCAACCGCAATGACATCATGCTGGTGAAGATGGCATCGCCAGTC 465
Qy 100 SerIleThrTrpAlaValArgProLeuThrLysSerSerArgCysValThrAlaGlyThr 119
Db 466 TCCATCACTGGGCTGTGCGACCCCTCACCTCTCTCTCACGCTGTGTCTCTGTGGCACC 525
Qy 120 SerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThr 139
Db 526 AGCTCCCTCATTTCCGGCTGGGCGACGACGCTCCAGCCCCCAGTTACGCTGCTCCACACC 585
Qy 140 LeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaThrProGly 159
Db 586 TTGGATCGGCAACATCACCATCATTTGAGCAGCAGAACGCTGTGAGAACGCTTACCCGGC 645
Qy 160 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 179
Db 646 AACATCACAGACCATGCTGTGCGCAGCTGTGAGGAGGGGCGGAGGACTCTCTGCCAG 705
Qy 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199
Db 706 GGTGACTCCGGGGGCCCTCTGCTGTAACTGCTCTTCAAGGCATTTATCTCTCTGGGGC 765
Qy 200 GlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysThrVal 219
Db 766 CAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTG 825
Qy 220 AspTrpIleGlnGluThrMetLysAsnAsn 229
Db 826 GACTGTGATCCAGGAGACGATGAAGAACAA 855
RESULT 7
US-08-790-137-2
; Sequence 2, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALLIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

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; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-835-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-790-137-2

Alignment Scores:
Pred. No.: 2,728-120 Length: 833
Score: 1213.00 Matches: 219
Percent Similarity: 97.82% Conservative: 5
Best Local Similarity: 95.63% Mismatches: 5
Query Match: 96.42% Indels: 0
DB: 0 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-790-137-2 (1-833)
QY 1 IleIleLysGlyPheGluCysLysProHisGlnProTrpGlnAlaAlaLeuPheGlu 20
DB 99 ATTGTGGAGGCTGGAGGTGTGAGCAGCATCCAGCCTGGCAGCGGCTCTGTACCAG 158
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
DB 159 AAGACGGCGTACTCTGTGGGGCGAGNFCATNGCCCGCAGATGTTCTTGACACAGCC 218
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 219 CACTGCTNAAGCCCGCTACATAGTTTACCTGGGGCAGCACAACCTCCAGAGGAGGAG 278
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
DB 279 GCGTGTGAGCAGACCCGAGCAGCAGTGTGCTCTCCCGCCAGCCCGGCTTCAACACAGC 338
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 339 CTCGCCCAACAGACACCCGCAATGACATCATGTGTTGATGATGGCATCGCCAGTCTCC 398
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 399 ATCACCTGGGCTGTGGAGCCCTCACCTCTCTCAGCGTGTGTCACTGCTGGCACCAGC 458
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
DB 459 TGCCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGCCAGTTAGCGCTGCTTCCACCTTG 518
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaIleProGlyAsn 160
DB 519 CGATGCGCCCAACATCACCATCATTGAGCACCAGAGAGTGTGAGAACGCTTACCCCGCAAC 578
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyCysLysAspSerCysGlnGly 180
DB 579 ATCACAGACACCATGTTGTGTGTCAGCGTGCAGGAGGGGGCAAGGACCTCTGCCAGGCT 638
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 639 GACTCCGGGGCCCTCTGTGTGTATACCAAGTCTCTTCAAGGCAATATCTCTCTGGGGCCAG 698
QY 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysThrValAsp 220
DB 699 GATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 758
QY 221 TrpIleGlnLysThrMetLysAsnAsn 229
DB 759 TGGATCCAGGAGCAGTGAAGAACAAAT 785

RESULT 8
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US-09-280-116-3  
; Sequence 3, Application US/09280116A  
; Patent No. 6331427

GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24, 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26

; NUMBER OF SEQ ID NOS: 268

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 3

; LENGTH: 618

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: trypsin-like serine proteases

US-09-280-116-3

Alignment Scores:

Pred. No.: 7,978-89 Length: 618  
Score: 916.50 Matches: 184  
Percent Similarity: 90.78% Conservative: 3  
Best Local Similarity: 89.32% Mismatches: 4  
Query Match: 72.85% Indels: 16  
DB: 4 Gaps: 2

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-280-116-3 (1-618)

QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaPro-ArgTrpLeuLeuThrAlaAlaHisCy 42

DB 2 CGGTACTCTGTGGGGGACC---TCATCGCTTCAGATGGCTCTGTGACAGAGCCCACTG 58

QY 42 sLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCy 62

DB 59 CCTCAAGCCCGCTTACATAGTTTACCTGGGGCAGCACAACCTCCAGAAAGGAGGAGGCTG 118

QY 62 sGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuPr 82

DB 119 TGACGACAGCCGGACGCCACTGAGTCTTCCCCCCCCCGGGCTTCAACACAGCCCTCCC 178

QY 82 oAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal-SerIle 102

DB 179 CAACAAGACCAACCGCATGACATCATGTGTTGATGATGGCATCGCCAGTGTCCATCA 238

QY 102 hrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysL 122

DB 239 CCTGGGCTGTGGAGCCCTCACCTCTCTCTCATGCTGTGTCACCTGTGGCACCAGCTGCC 298

QY 122 euIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeuArgC 142

DB 299 TCATTTCCGGCTGGGGCAGCAGCTTCAGCCCCCAGTTACGCTTGCCTCACACCTTGGAT 358

QY 142 ysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaIleProGlyAsnIle 162

DB 359 CGGCCAACATCACCATCATTTGAGCACCAGAGTGTGAGAACGCCCTTACCCCGCAACATCA 418

QY 162 hrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAsps 182

DB 419 CAGACACCATGTTGTGCGCAGCGTGAAGGAGGGGGCAAGGACTCTTGCCTCTCTGCAA 471

QY 182 erGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp-GlyGlnAsp 201

DB 472 -----GTCTCTTC-AAAGGCATTATCTCTCTGGGGGCGCAGGAC 507

QY 202 -ProCysAlaIleThrArgLysProGlyValThrLysValCysLysThrValAspTr 221

DB 508 TCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTGGACTG 567

QY 221 pileGlnGlu 224

DB 568 GATCCAGGAA 577





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QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db 612 CACTGTAAAAAACCAGAAATACACAGTACGCTGGGAGACACACAGCTACAGAAATAAGAT 553
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db 552 GGCCACAGACAGAAATACCTGTGTTGATGCTCATCCACACCCCTGTCTACACAGCAGC 493
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 492 ---GATGTGGAGGACACCAACCATGATCTGATGCTTCTCACTGGGTGACCGCATCC 436
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 435 CTGGGTCCAAAGTGAAGCCCATCAGCTGGCAGATCATTCACCCAGCAGCTGGCCAGAG 376
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db 375 TGCACCGTCTCAGCTGGGCACTGTCCACAGTCCCGGAGAAATTTCTGACACTCTC 316
QY 141 ArgCysAlaAsnIleThrIleLeuGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db 315 AACTGTGCAGAGTAAATTTTCCAGAGAAAGTGTGAGATGCTTACCCGGGGCAG 256
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180
Db 255 ATCAGAGATGGCATGTCTGTGAGGACGACGACGAAAGGGCT---GACACGTGCCAGGC 199
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 198 GATTCGTGGAGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 139
QY 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 220
Db 138 GACCCCTGTGGAGGTCAGCAAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGAC 79
QY 221 TrpIleGlnGlu 224
Db 78 TGGATCAAGAAG 67

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RESULT 11

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US-09-618-259-6
; Sequence 6, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 6
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding Tumor Antigen Derived
; OTHER INFORMATION: Gene-14 (TAGD-14) protein; nt 1344-1360 NCBI accession
; OTHER INFORMATION: #AA343629
US-09-618-259-6

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Alignment Scores:
Pred. No.: 3,69e-63 Length: 1360
Score: 681.00 Matches: 116
Percent Similarity: 70.54% Conservative: 42
Best Local Similarity: 51.79% Mismatches: 64
Query Match: 54.13% Indels: 2
DB: 4 Gaps: 2
US-09-856-320a-2_COPY_54_282 (1-229) x US-09-618-259-6 (1-1360)

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QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20
Db 612 GTGTGGGGGTCTCATGAGTGCACCAACCCATTCGCAGCCTTGGCAGGCGCTTGTTCAG 671
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
Db 672 GGCCACAGCAACTACTCTGTGGCGGTGCTCTGTAGTGGCAACTGGGTCTTACAGCTGCC 731
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db 732 CACTGTAAAAAACCAGAAATACACAGTACGCTGGGAGACACACAGCTACAGAAATAAGAT 791
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db 792 GGCCACAGCAGCAAGAAATACCTGTGTTTCACTGCTCCATCCACCCCTGTCTACACAGCAGC 851
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 852 ---GATGTGGAGGACCAACCATGATGCTTCTTCACTGCTGGTGTGACCGCATCC 908
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 909 CTGGGGTCCAAAGTGAAGCCCATCAGCTGGCAGATCATTCACCCAGCCTGGCCAGAG 968
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db 969 TGCACCGTCTCAGCTGGGCACTGTCCACAGTCCCGGAGAGATTTTCTGACACTCTC 1028
QY 141 ArgCysAlaAsnIleThrIleLeuGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db 1029 AACTGTGCAGAGTAAATTTTCCAGAGAAAGTGTGAGGATGCTTACCCGGGGCAG 1088
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db 1089 ATCAGATGTCATGTCTGTGAGGACGACGACGAAAGGGCT---GACACGTGCCAGGC 1145
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 1146 GATTCGTGGAGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1205
QY 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 220
Db 1206 GACCCCTGTGGAGGTCAGCAAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGAC 1265
QY 221 TrpIleGlnGlu 224
Db 1266 TGGATCAAGAAG 1277

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RESULT 12

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US-09-008-271A-19
; Sequence 19, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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Thu Jun 24 10:06:29 2004

Job time : 99 secs

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1364)
; OTHER INFORMATION: n = a, t, c, or g
US-09-280-116-20

Alignment Scores:
Pred. No.:      3.43e-58      Length:      1364
Score:          634.50        Matches:      123
Percent Similarity: 64.82%    Conservative: 41
Best Local Similarity: 48.62% Mismatches:      60
Query Match:      50.44%      Indels:       29
DB:               4          Gaps:         3

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-280-116-20 (1-1364)

Qy      4  GlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArg 23
Db      828 GGCTACACCTGCTTCCCCCACTCTCAGCCCTGCGAGGCTGCCCTACTAGTGAAGGGCGG 769

Qy      24  LeuLeuCysGlyAlaThr-LeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLe 43
Db      768 CTACTCTGTGGGGAAGTCTGTGTCACCCCAATGGGTCTCCTACTGCCGCCACACTGTCT 709

Qy      43  uLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGl 63
Db      708 AAGGAGGGGCTCAAAAGTTTACCTAGGCAAGCAGCCCTAGGGCGTGTGAAAGCTGGTGA 649

Qy      63  uGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAs 83
Db      648 GCAGGTGAGGGAAGTGTGTCACCTATCCCCCACTGATCCCGGAGAGGCCCCACCCCA 589

Qy      83  nLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTr 103
Db      588 CTTGAACCAACCATGACATCATGCTTCTGGAGCTGCAGTCCCGGTCACAGTCACAGG 529

Qy      103  pAlaValArgProLeuSer---SerArgCysValThrAlaGlyThrSerCysLe 122
Db      528 CTACATCCAAACCTGCGCTTTCCCAACACACCCCTAACCCCTGGCACCACCTGTGG 469

Qy      122  uIleSerGlyTrpGlySerSerSerProGln-----LeuAr 135
Db      468 GGTGCTGGCTGGGGACCAACACCAAGCCCGGATGTCACCCACACAGGTGCTGAG 409

Qy      135  g-----Le 136
Db      408 GCCCATAGGAGTGGTGGGAAACACAGGGGAGAGATGGGAGGAAGTCTGAGTGAATT 349

Qy      136  uProHis-ThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnA 156
Db      348 ACCCAAAACTTACAAATGTCACCAATCCAACTTCCTCAGATGAGGAGTGTCTGCAAG 289

Qy      156  latYrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLea 176
Db      288 TCTACCCAGGAAGATCACTGACACATGTTGTGTCGGGCACAAAGAGGGTGGCAAG 229

Qy      176  spSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIleI 196
Db      228 ACTCCTGTGAGGTGACTCTGGGGGGCCCTGTGCTGTAAACAGAACTGTATGGCATCG 169

Qy      196  leSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLysValC 216
Db      168 TCTCCTGGGAGACTTCCCATGTGGGCAACCTGACCGGCTGTGTCTACACCCGTGTCT 109

Qy      216  ysLysTyrValAspTrpIleGlnGluThrMetLys 227
Db      108 CAAGATACGTCCTGTGGATCCGTGAACAATCCGA 74

```

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 01:21:03 ; Search time 2957 Seconds  
(without alignments)  
2312.627 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IIKGPECKPHSQPWAALFE.....GYVTKVKYVDVIQETMKKN 229

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856320 @CEN 1.1 6425 @runat\_22062004\_172806\_11879 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_rus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223.5	97.3	1282	11	BC015551 Homo sapi
2	1158	92.1	841	12	BI818697
3	1146	91.1	678	12	BI783040
4	1141	90.7	853	12	EG720793
5	1112.5	88.4	1072	12	BM559782
6	1062	84.4	1295	11	AK009360 Mus muscu
7	1062	84.4	1295	11	AK009720 Mus muscu
8	1061.5	84.4	1074	12	BM559617
9	1036	82.4	1269	11	AK009659
10	1008	80.1	753	29	AY410892 Homo sapi
11	992	78.9	556	29	AY410893 Pan trogl
12	958	76.2	708	12	EG697071
13	895	71.1	592	14	CF768612
14	852	67.7	639	12	BF747134
15	834	66.3	556	29	AY410894 Mus muscu
16	792.5	63.0	973	10	BE867930
17	780	62.0	761	12	BM982377
18	775	61.6	528	13	EX528424
19	744.5	59.2	747	13	EX109836
20	724	57.6	467	9	AI893370
21	720	57.2	467	9	AA073833
22	684	54.4	783	29	AY410900 Mus muscu
23	684	54.4	880	14	CB202840
24	681	54.1	783	29	AY410898 Homo sapi
25	678	53.9	898	14	CB204935
26	664	52.8	539	12	BM837078
27	664	52.8	852	14	CB587168
28	657	52.2	783	29	AY410899 Pan trogl
29	639	50.8	826	14	CB574882
30	630	50.1	1048	11	AK004807
31	626	49.8	673	13	BU684799
32	623.5	49.6	1240	11	AK003996
33	620.5	49.3	368	9	AA412318
34	607	48.3	451	14	W60374
35	603	47.9	754	12	BI653899
36	598.5	47.6	966	13	BY709314
37	598	47.5	765	13	BU488441
38	597.5	47.5	890	11	AK009217
39	597	47.5	801	13	BU417451
40	595	47.3	766	13	BU416879
41	595	47.3	786	13	BU416290
42	595	47.3	793	13	BU487643
43	595	47.3	808	13	BU416510
44	595	47.3	810	13	BU417474
45	595	47.3	811	13	BU417330

# ALIGNMENTS

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LOCUS BC015551 1282 bp mRNA linear HTC 17-DEC-2003  
DEFINITION Homo sapiens cDNA clone IMAGE:3847565, containing frame-shift errors.  
ACCESSION BC015551  
VERSION BC015551.2 GI:34190438  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1282)

AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bueckow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullay, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahezy, J., Helton, E., Kettaman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PubMed	12477932
REFERENCE	2 (bases 1 to 1282)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> On Aug 25, 2003 this sequence version replaced gi:15930236. Contact: MGC help desk Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	source Location/Qualifiers 1..1282 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3847565" /tissue_type="Colon, adenocarcinoma" /clone_lib="NIH_MGC_65" /lab_host="DH10B" /note="vector: pcwv-sport6"
ORIGIN	
Alignment Scores:	
Pred. No.:	6.02e-113
Score:	1223.50
Percent Similarity:	99.13%
Best Local Similarity:	98.70%
Query Match:	97.26%
DB:	11
US-09-856-320A-2_COPY_54_282 (1-229) x BC015551 (1-1282)	
Qy	1 llelellysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20 

Db	266	ATCATGAAGGGTTCGAGTCAAGACCTCACTCCAGCCCTGGCAGCGCCCTGTTCAAG	325
Qy	21	LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla	40
Db	326	AAGACGGGGTACTCTGTGGGGGACGCTCATCGCCCAAGATGGCTCTCGACAGCAGCC	385
Qy	41	HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysG	59
Db	386	CACCTGCCCTCAAGCGGTGGCGCTACATAGTTCACTTGGGGCAGCACAACCTCCAGAA	445
Qy	59	uGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAs	79
Db	446	GGAGGGCTGTGACGACACCGCGACCATCTGAGTCTCTCCCAACCCCGGCTTCAACAA	505
Qy	79	nSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVa	99
Db	506	CAGCCTCCCAACAACACCGCAATGACATCATCTGGTGAAGATGCGATCGCCAGT	565
Qy	99	lSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyTh	119
Db	566	CTCCATCACCTGGGCTGTGGACCCCTCACCCCTCTCTCAGCTGTGTCTACTGCTGGC	625
Qy	119	rSerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisTh	139
Db	626	CAGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGCAGTTACGCTGCTCACAC	685
Qy	139	rLeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyProGl	159
Db	686	CTTCGATCGGCCAACATCACCATTGAGCAGCAGAGTGAGAACCCCTACCCCGG	745
Qy	159	yAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysG	179
Db	746	CAACATACAGACACCATCTGTGTGCCGGTGCAGAGGGGGCAGGACCTCTGCCA	805
Qy	179	nGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpG	199
Db	806	GGGTGACTCCGGGGGCTCTGTGTCTGTAAACCATCTCTTCAAGGCATTATCTCTGG	865
Qy	199	yGlnAspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyVa	219
Db	866	CCAGATCCGTGCGATCACCCGAAAGCCCTGTGTCTACACGAAAGTCTGCAATATGT	925
Qy	219	laspTrpIleGlnGluThrMetLysAsnAsn	229
Db	926	GGACTGGATCCAGGACGATGAAGACAAT	956
RESULT 2			
Bi18697			
LOCUS	603037514F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178746 5',		
DEFINITION	mRNA sequence.		
ACCESSION	BI18697		
VERSION	BI18697.1 GI:15930247		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 841)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11445 row: k column: 03 High quality sequence stop: 784.		

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FEATURES
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Location/Qualifiers
1..841
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:518746"
/lab_host="DH10B"
/clone_lib="NIH_MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1,27e-106 Length: 841
Score: 1158.00 Matches: 222
Percent Similarity: 97.38% Conservative: 1
Best Local Similarity: 96.94% Mismatches: 1
Query Match: 92.05% Indels: 5
DB: 12 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x BI818697 (1-841)

QY 6 GluCysLysProHisSerGln-ProTrpGlnAlaLeuPheGluLysThrArgLeuLe 25
Db 2 GAGTGCAGCCCTCACTCCAGTCCCTGGCAGGAGCCCTGTTCGAGAGAGCGCGCTACT 61

QY 25 uCysGlyAlaThrLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysPr 45
Db 62 CTGTGGGGGCGAGCTCATCGCCCCAGATGGTCTCTGACAGAGCCCACTGCCTCAAGCC 121

QY 45 oArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnTh 65
Db 122 CGGTACATAGTTCACCTGGGGCAGCAACACCTCCAGAGGAGGAGGCTGTGACAGAC 181

QY 65 rArg-ThrAlaThrGluSerPheProHisProGlyPheAsnAspSerLeuProHisLysA 85
Db 182 CTGTGACAGCCCACTGAGTCTTCCCGCCACCGGGTTCACACAGAGCTCCCAACAAG 241

QY 85 sPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer-IleThrTrpAla 104
Db 242 ACCACCGCAATGACATCATGCTGGTGAAGATGGCATGCCAGTCTCTTATCACCTGGGCT 301

QY 105 ValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLysSer 124
Db 302 GTGGACCCCTCACCTCTCTCACGCTGTGTCATGCTGGACACGAGTGCCTCATTTCC 361

QY 125 GlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsn 144
Db 362 GSCTGGGGCAGCAGCTCCAGCCCCAGTACGCTGCTCTCACCTTGCAGTGGCCAC 421

QY 145 IleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThr 164
Db 422 ATCCACCATATTGAGCACCAGAGGTGTGAGAACGGCTACCCCGGCAACATCACAGACAC 481

QY 165 MetValCysAlaSerValGlnGlu-GlyGlyLysAspSerCysGlnGlyAspSerGlyG 184
Db 482 ATGGTGTGTGCCAGGTGCAGAGAGGGGGCAAGGACTCTCTGCCAGGTGACTCCGGGG 541

QY 184 yProLeuValCysAsnGlnSerLeuGln-GlyIleIleSerTrpGlyGlnAspProCysA 204
Db 542 CCTCTGTGTGAACCACTCTCTCAATGGCATTTATCTCTGGGGCCAGGATCCGTGTG 601

QY 204 lIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGln 224
Db 602 CGATCCCGAAAGCCTGGTGTACACGAAAGTCTGCAATATATGTGAGTGGATCCAGG 661

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QY 224 luThrMetLysAsnAsn 229
Db 662 AGACGATGAAGACAAT 678

RESULT 3
BI763040
LOCUS BI763040
DEFINITION 603047838F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187896 5',
BI763040 mRNA sequence.
VERSION BI763040
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 678)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaops-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11469 row: h column: 09
High quality sequence stop: 647.
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/db_xref="taxon:9606"
/clone="IMAGE:5187896"
/lab_host="DH10B"
/clone_lib="NIH_MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1,44e-105 Length: 678
Score: 1146.00 Matches: 210
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 1
Query Match: 91.10% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x BI763040 (1-678)

QY 19 PheGluLysThrArgLeuLeuCysGlyAlaThrLeuAlaProArgTrpLeuLeuThr 38
Db 10 TTCGAGAGACGGGGTACTCTGTGGGGGAGCTCATGCCGCCAGATGGCTCTCGACA 69

QY 39 AlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
Db 70 GCAGCCCACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCAGCACTCCAGAG 129

QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78

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130 GAGGAGGCTGTGACGAGACCCGGACAGCAGCAGCTGAGTCTCTCCGCCACCCCGGCTTCAAC 189  
 QY 79 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 98  
 Db 190 AACAGAGCTCCCAACAAACAGCAGCAGCATGACATCATCTGCTGGAAGATGGCATCGCCA 249  
 QY 99 valSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 118  
 Db 250 GTCTCCATCACCTGGGCTGTGGACCCCTCACCCCTCTCTCCAGCTGTGTCCTCTGGC 309  
 QY 119 ThrSerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHis 138  
 Db 310 ACCAGTGGCTCATTTCCGGCTGGGCGCAGCAGTCCAGCCCCCAGTTACGCTGCTCAC 369  
 QY 139 ThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnIleThrPro 158  
 Db 370 ACCTTGGATGCGCCCAACATCACCATCATTTGAGCAGCAGAGTGTGAGAACCCCTACCCC 429  
 QY 159 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyCysAspSerCys 178  
 Db 430 GGCACATCACAGACCATGTGTGTGCGGTGCGAGAGGGGCGAGGACTCTCTGC 489  
 QY 179 GlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 198  
 Db 490 CAGGTTGACTCCGGGGGCTCTGTGTCTGTAAACAGTCTCTTCAAGGCAATTATCTCCTGG 549  
 QY 199 GlyAlaAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrp 218  
 Db 550 GGCAGAGATCCGTGTGGATCACCCGAAAGCCCTGTGTCTACAGGAAGTCTGCAATAT 609  
 QY 219 ValAspTrpIleGlnGluThrMetLysAsnAsn 229  
 Db 610 GTGCACTGGATCCAGGAGCAGTGAAGAACAAT 642

RESULT 4  
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 LOCUS 602692015F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4824387 5',  
 DEFINITION mRNA sequence.

ACCSSION BG720793.1 GI:13999980  
 VERSION BG720793  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 853)  
 NTH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14M10735 row: n column: 04  
 High quality sequence stop: 826.

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 /clone="IMAGE:4824387"  
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 (gtcag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
 insert size 2.2 kb and normalized to ROT 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NIH/NHGRI, National Institutes of Health). Note: this is  
 a NIH\_MGC Library."

ORIGIN  
 Alignment Scores: Length: 853  
 Pred. No.: 1141.00 Matches: 216  
 Score: 1141.00 Conservative: 0  
 Percent Similarity: 98.18% Mismatches: 3  
 Best Local Similarity: 98.18% Indels: 2  
 Query Match: 90.70% Gaps: 0  
 DB: 12

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BG720793 (1-853)  
 QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
 Db 196 ATCATCAAGGGTTCGAGTCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCGAG 255  
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40  
 Db 256 AAGACGGGGTACTCTGTGGGGGAGCCTCATCGCCCGGAGATGGCTCTCTGACGAGGCC 315  
 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
 Db 316 CACTGCCCTCAAGCCCGCTACATAGTTCACTGGGGCAGCACCACTCCAGAGAGGAGGAG 375  
 QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80  
 Db 376 GGCTGTGAGCAGACCCGGACAGCAGTCACTGCTTCCCGCAGCCGGCTTCAACACACAGC 435  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 436 CTCGCCAACAAAGACCCGCAATGATCATGCTGTGTGAAGATGGCATCGCCAGTCTCC 495  
 QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 496 ATCACTGGGGTGTGGACCCCTCACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555  
 QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 556 TGCCTCATTTCCGGCTGGGCGCAGCAGCTCAGCCCCCAGTACGCTGCTCTCACCTTG 615  
 QY 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaIleThrProGlyAsn 160  
 Db 616 CGATGCGCCACATCACCATCATTTGAGCAGCAGAGTGTGAGAACGCTTACCCCGGCAAC 675  
 QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180  
 Db 676 ATCAAGACACCATGGTGTGGCAGCGTGCAGGAAGGGGCAAGGACTCTCTGCGCAGTT- 734  
 QY 181 AspSerGlyGlyProLeuVal-CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGly 200  
 Db 735 GACTCCGGGGCCCTCTGGTCTTGTAAACAGTCTCTTCAAGGCAATTATCTCTGGGTGCA 794  
 QY 200 nAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrpVal 219  
 Db 795 GGATCCGTGTGCGATCACCCGAAAGCCCTGTGTCTACACGAAGTCTGCAATATGTG 852

RESULT 5  
 BM559782 1072 bp mRNA linear EST 20-FEB-2002  
 LOCUS BM559782  
 DEFINITION AGENCOURT\_6565460 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5744410  
 5', mRNA sequence.  
 ACCSSION BM559782  
 VERSION BM559782.1 GI:18803655  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1072)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgaabp-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Place: LLNL2765 row: 1 column: 11  
High quality sequence stop: 684.

## FEATURES

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Location/Qualifiers

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/organism="Homo sapiens"  
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/tissue\_type="medulla"  
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/clone\_lib="NIH MGC 119"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 7,9e-102 Length: 1072  
Score: 1112.50 Matches: 212  
Percent Similarity: 95.54% Conservative: 2  
Best Local Similarity: 94.64% Mismatches: 7  
Query Match: 88.43% Indels: 3  
DB: 12 Gaps: 1

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BM559782 (1-1072)

QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
DB 275 ATCATCAAGGGTTCAGTGCAGGCTCACTCCAGCCCTGCAGCGAGCCTGTTCAG 334  
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThraAla 40  
DB 335 AAGACGGGGCTACTCTGTGGGCGGACGCTCATCGCCCCAGATGCTCTGCACAGCACC 394  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
DB 395 CACTGCCCTCAAGCCCGCTACATAGTTCACTGGGGGAGCAACCTCCAGAGGAGGAG 454  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 455 GCCTGTGAGCAGACCCGGACACCCACTGAGTCTTCCCCCGCCCGGCTTCAACACAGC 514  
QY 81 LeuProAsnLysAspHisArgAsnAspLeuMetLeuValLysMetAlaSerProValSer 100  
DB 515 CTCCTCCCAACAAACACCGCAATGACATCATGCTGGTGAAGATGGCATCGCCAGTCTCC 574  
QY 101 lleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 575 ATCACTGNGCTGTGGACCCCTCACTCTCCTCAGCTGTGTGCTGCTGGACACAGC 634  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140

Db 635 TGCCTCATTTCCGCTGGGCGACGACGCTCCAGCCCCAGTTACGCTGCTCACACCTTG 694  
QY 141 ArgCysAlaAsnIleThrIlelleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
Db 695 CGATGCGCCCAACATCACCATTCATTGACACACAGAGTGTGAGAACGCTACCCCGGCAC 754  
QY 161 IleThrAspThrMetValCysAlaSerValGlnIleGlyGlyLysAspSerCysGlnGly 180  
Db 755 ATCACACACACCATGGTGTGTGCCAGCGTGCAGAAAGGGGCGAGGACTCCTGCNCAGGT 814  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly-G1 200  
Db 815 GACTCCGGGGGCGCTCTGGTCTGTATACCAAGTCTCTTCAAGGCATTATCTCTGGGGCCCA 874  
QY 200 nAspProCysAlaIleThrArgLysProGlyValTyrThr---LysValCysLysTyrVa 219  
Db 875 GGATCCGCTGTGCGATCACCCGAAAGCCTGTGTCTACCCGAAAGGCTGTGCCAATATGT 934  
QY 219 1-AspTrp 221  
Db 935 GGGACTCG 942  
RESULT 6  
AKO09360 1295 bp mRNA linear HTC 20-SEP-2003  
LOCUS Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
DEFINITION library, clone:2310015I08 product:protease, serine, 20, full insert  
sequence.  
ACCESSION AKO09360  
VERSION AKO09360.1 GI:12844110  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 15-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Sugahara,Y., Shibata,K.,  
Itoh,N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
3  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuami,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Hatada,A.,  
Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,U.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)



TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Okawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1295)

ADACHI, J., AIZAWA, K., AKAHIRA, S., AKIMURA, T., ARAI, A., AONO, H.,  
ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y.,  
HIRANO, M., HANAGAKI, T., HARA, A., HAYATSU, N., HIRAMOTO, K.,  
FURUKAWA, T., HORI, P., IMORANI, K., ISHII, Y., ITOH, M., IZAWA, M.,  
KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KONNO, H., KOUNDA, M.,  
KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., NISHI, K.,  
NOMURA, K., NUMAZAKI, R., OHNO, M., OKAZAKI, Y., OKIDO, T., OWA, C.,  
SAITO, H., SAITO, R., SAKAI, K., SAKAI, K., SANO, H., SASAKI, D.,  
SHIBATA, K., SHIBATA, Y., SHINAGAWA, A., SHIRAKI, T., SOGABE, Y.,  
SUZUKI, H., TAGAMI, M., TAGAWA, A., TAKAHASHI, P., TANAKA, T.,  
TEJIMA, Y., TOYA, T., YAMAMURA, T., YASUNISHI, A., YOSHIDA, K.,  
YOSHINO, M., YURAMATSU, M. and HAYASHIZAKI, Y.  
Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

CDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using triphosphate thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. Second  
strand cDNA was prepared with the primer adapter of sequence [5'  
GAGAGAGAGATCCAGCTTAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved  
with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.  
Host: SOLR.

Location/Qualifiers  
1. .1295  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CS7BL/6J"  
/db\_xref="PANTOM\_DB:2310040F07"  
/db\_xref="MGI:1898372"  
/db\_xref="taxon:10090"

FEATURES  
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/clone="2310040F07"  
/sex="male"  
/tissue\_type="tongue"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="adult"  
144. .974  
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(MGI:MGI:1929977)  
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/db\_xref="GI:26365926"  
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ETRIKGEORPHSQPQVALFAPKLLTLCATLAPKLLTAARCKRPHVILVLSHN  
LEKTDCEORRMATEFPHDPNNSLPNKDRNDIMLVKMSVPFCTRAVQPLTSPH  
CYAAGTSCILISGNGTSSPOLRLPHSLRCANVSILIEHKCEKAYPGNIDTLMCASVR  
KEGRDSCQSGDGGGLVNGSLQGLIISWGQDPCAVTRKPGVITKVKFFRWIHEVMERN  
"

ORIGIN  
Alignment Scores:  
Pred. No.: 1,44e-96 Length: 1295  
Score: 1062.00 Matches: 186  
Percent Similarity: 91.27% Conservative: 23  
Best Local Similarity: 81.22% Mismatches: 20  
Query Match: 84.42% Indels: 0  
DB: 11 Gaps: 0  
US-09-856-320A-2\_COPY\_54\_282 (1-229) x AK009720 (1-1295)

Oy 1 IlellelysglypheglucyslysProHisserGlnProTrpGlnAlaAlaLeuPheGlu 20  
Db 285 ATCATCAAGGTTATGAGTCAGCGCCCTCACTCAGCCATGCGAGGTGGCCCTTTTCAG 344  
Oy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
Db 345 AAGACACGGTTCTCTGTGGGGCAACCTCATGCCCCCAATGGCTCTCTGACAGAGCC 404  
Oy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
Db 405 CACTGCCGCAAGCCCATACGTGATCTCTTGGAGAGCACAATCTAGAGAAGACAGAC 464  
Oy 61 GlyCysGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80  
Db 465 GGCTGTGAGCAGAGCGGATGGCCACTGAGTCTCTCCCCACCCGACTTCAACACAGC 524  
Oy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 525 CTCCCCAACCAAGACACCCGATGACATAATCTGTGAAGATGCTGCTCCGCTTC 584  
Oy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 585 TTATCCCGAGCTGTGACGCACTCACCTGTCTCCACACCTGCTCGTCGAGGCACGAC 644  
Oy 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
Db 645 TGCTCTATTTCTGAGTGGGCACACGTCAGCCGCTTCGCTGCTCTCTCTCTT 704  
Oy 141 ArgCysAlaAsnLeuThrIleLeuGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
Db 705 CGATGTGCCAATGCTCCATCATCGAACACAGAGGTGTGAGAAGGCTTACCCGGGCAAC 764  
Oy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180  
Db 765 ATACAGACACCATGCTGTGCGCAGTTCGGAAGAGGGCGAGGACTCTGTCAGGGT 824  
Oy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 825 GACTCTGAGGCCCTCTGTCTGCAACGGATCTCTTCAAGGCATCATCTCTCGGGTCAG 884  
Oy 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
Db 885 GACCCATGTCCTGTCACCAAGAGCGCTGGTGTCTATACAAAAGTGTGCAAAATCTTAAAC 944



JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861	Pred. No.: 6.01e-94 Score: 1036.00 Percent Similarity: 91.27% Best Local Similarity: 80.79% Query Match: 82.35% DB: 11	Length: 1269 Matches: 185 Conservative: 24 Mismatches: 20 Indels: 1 Gaps: 0
TITLE JOURNAL REFERENCE AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 695-690 (2001)	US-09-856-320A-2_COPY_54_282 (1-229) x AK009659 (1-1269)	
TITLE JOURNAL REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	QY 1 IlelelysglyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20 Db 260 ATCATCAAGGTTATGAGTGCAGGCTCACTCAGCAGCATGCGAGTGGCCTCTTTTCAG 319 QY 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40 Db 320 AAGACAGCGCTTCTCTGTGGGCAACCTCATGCCCCCAATGGCTCTTCAGACAGCC 379 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60 Db 380 CACTGCCGCAAGCCCATTCAGTGTCTCTTGGAGAGCAGCAATCTAGAGAGACAGAC 439 QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80 Db 440 GGCTGTGAGCGAGG-CGGATGGCCACTGAGTCTTCCCCCAGCCGACTTCAACACAGC 499 QY 81 LeuProAsnLysAspHisArgAsnAspIleValLeuValLysMetAlaSerProValSer 100 Db 499 CTCCCCAACAAAGACACCGAATGACATAATGCTTGTGAGATGCTCTCCCGTCTTC 558 QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120 Db 559 TTTACCCGAGCTGTGCACCACTCACCTGTCTCCCACTGTGTGCTGCAGGACAGC 618 QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140 Db 619 TGCTTCATTTCTGGATGGGCAACGCTCCAGCCCGCAGTGGCTTCCTCATTCCTTG 678 QY 141 ArgCysAlaAniIleThrIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160 Db 679 CGATGTGCCAATGCTCCATCATCGAACACAAAGAGTGTGAGAGGCTACCCGGGCAAC 738 QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyCysAspSerCysGlnGly 180 Db 739 ATCAGACACACATGCTGTGGCCAGTGTTCGGAAGAGGCGGCAAGGACTCTGTGAGGT 798 QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200 Db 799 GACTCTGGAGCCCTGGTCTGCACGGATCTCTTCAAGGCATCATCTCTCTGGGTGAG 858 QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValasp 220 Db 859 GACCCATGTCCGTCACAGAAAGCTGTGTCTATACAAAGTCTGCAATACTTTTAA 918 QY 221 TrpIleGlnGluThrMetLysAsnAsn 229 Db 919 TGGATCCAGAGGTTATGAGGAAACAAT 945	
FEATURES Source	Location/Qualifiers 1..1269 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:2310037E23" /db_xref="MGI:1894042" /db_xref="taxon:10090" /clone="2310037E23" /sex="male" /issue_type="tongue" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 119..948 /notes="protease, serine, 20 (MGD MGI:1929977) putative" polyA_signal 1251..1256 /note="putative" polyA_site 1269 /notes="putative"	RESULT 10 AY410892 LOCUS DEFINITION Homo sapiens KLK11 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION AY410892 VERSION AY410892.1 GI:39766860 KEYWORDS GSS. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 753) Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,	
TITLE JOURNAL REFERENCE AUTHORS	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTATTAATATCCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.		
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polyA_signal	1251..1256 /note="putative"		
polyA_site	1269 /notes="putative"		
ORIGIN			
Alignment Scores:			

Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 JOURNAL  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 753)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 FEATURES  
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 1..753  
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 Alignment Scores:  
 Pred. No.: 1.68e-91 Length: 753  
 Score: 1008.00 Matches: 184  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.13% Indels: 0  
 DB: 29 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AY410892 (1-753)  
 QY 46 ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThr 65  
 DB 199 CGTACATAGTTACCTGGGGGAGCAGACCACTCCAGAGGAGGGCTGTGAGCAGACC 258  
 QY 66 ArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAsp 85  
 DB 259 CGGACAGCCACTGAGTCTCTCCCGCCACCCCGGCTTCAACAACAGCCCTCCCAACAAAGAC 318  
 QY 86 HisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaVal 105  
 DB 319 CACCGCAATGACATCATCTGTGTGAGATGGCATCGCCAGTCTCCATCATCCTGGGCTGTG 378  
 QY 106 ArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysteuleSerGly 125  
 DB 379 CGACCCCTCACCTCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGC 438  
 QY 126 TrpGlySerThrSerProGlnLeuArgCysValThrProHisThrLeuArgCysAlaAsnIle 145  
 DB 439 TGGGGGAGCAGCTCCAGCCCCCAGTTACGCTCCCTCCACACCTTGCATGCGCCCAACATC 498  
 QY 146 ThrIleIleGluHisGlnLysCysGluAsnAlaThrProGlyAsnIleThrAspThrMet 165  
 DB 499 ACCATCATTCAGCACCCAGAGAGTGTGAGACCGCTACCCCGGCAACATCACAGACCAATG 558  
 QY 166 ValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyPro 185  
 DB 559 GTGTGTGCCAGCTGTGAGGAGGGGCGAGGACTCTCTGCGAGGGTACATCCCGGGGCGCT 618  
 QY 186 LeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 205  
 DB 619 CTGGTCTGTAAACAGTCTCTCAAGCAATATCTCTCTGGGGCCAGGATCCGTTGGCATC 678  
 QY 206 ThrArgLysProGlyValThrThrLysValCysLysThrValAspTrpIleGlnGluThr 225  
 DB 679 ACCCGAAAGCTGTGTCTACACGAAAGTGTGAAATATGTGACTGTGATCCAGGAGAGG 738  
 QY 226 MetLysAsnAsn 229  
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Db 739 ATGAAGAACAAAT 750  
 RESULT 11  
 AY410893  
 LOCUS  
 DEFINITION Pan troglodytes KLX11 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY410893  
 VERSION AY410893.1 GI:39766861  
 KEYWORDS GSS  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 REFERENCE 1 (bases 1 to 556)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 1..556  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
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 /gene="KLX11"  
 /locus\_tag="HCM4042"  
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 Alignment Scores:  
 Pred. No.: 4.17e-90 Length: 556  
 Score: 992.00 Matches: 180  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 97.83% Mismatches: 0  
 Query Match: 78.86% Indels: 0  
 DB: 29 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AY410893 (1-556)  
 QY 46 ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThr 65  
 DB 2 CGCTACATAGTTACCTGGGGGAGCAGACCACTCCAGAGGAGGGCTGTGAGCAGACC 61  
 QY 66 ArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAsp 85  
 DB 62 CAGACAGCCACTGAGTCTCTCCCGCCACCCCGGCTTCAACGACAGCTCCCAACAAAGAC 121  
 QY 86 HisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaVal 105  
 DB 122 CACCGCAATGACATCATCTGTGTGAGATGGCATCGCCAGTCTCCATCATCCTGGGCTGTG 181  
 QY 106 ArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysteuleSerGly 125  
 DB 182 CGACCCCTCACCTCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGC 241  
 QY 126 TrpGlySerThrSerProGlnLeuArgLysProHisThrLeuArgCysAlaAsnIle 145  
 DB 242 TGGGGGAGCAGCTCCAGCCCCCAGTTACGCTGCCTCACACCTTGGATCGCCCAACATC 301  
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Site 2: Xho I; Library made from pooled skin of adult female Hereford-Shorthorn."

## ORIGIN

Alignment Scores:  
Pred. No.: 3,15e-80 Length: 592  
Score: 895.00 Matches: 156  
Percent Similarity: 92.27% Conservative: 23  
Best Local Similarity: 80.41% Mismatches: 15  
Query Match: 71.14% Indels: 0  
DB: 14 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x CF768612 (1-592)

Qy 36 LeuLeuThrAlaAlaHisCysLeuLeuProArgTyrIleValHisLeuGlyGlnHisAsn 55  
Db 2 CTTCTGACAGCAGCCACTGCGCAGCCCGATATGTGTTTACCTGGGAGCGCACAGC 61  
Qy 56 LeuGlnLysGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisPro 75  
Db 62 CTCGGGCGGAGGATGCTGTGACAGACGACGAACTGCCAACAGTCTTCCCGCCACCA 121  
Qy 76 GlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMet 95  
Db 122 GACTTCAACAACAGCTCCCAACAAGACCCAGCAACGACATCATGCTGGTGAAGATG 181  
Qy 96 AlaSerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysVal 115  
Db 182 GTGACCCCGCCACCTCCTGCGCTGTGCGACCCCTCACCCTGTCACCGCGCTGTG 241  
Qy 116 ThrAlaGlyThrSerCysLeuLeuSerGlyTrpGlySerThrSerProGlnLeuArg 135  
Db 242 CCTGCTGTGCCAATGCCCTCATTTCCGGCTGGGGCACCATGTCACAGCCCCAGTTGCAC 301  
Qy 136 LeuProHisThrLeuArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsn 155  
Db 302 CTGCCCCATACCTTGGCATCGCCACAGTCACCATCATCAAGCACAGGAGTGTGAGGAC 361  
Qy 156 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLys 175  
Db 362 GCCTACCTCGCAACATCAGCACACCATGTGTGTGTCAGTGTCCGCAAGAGGCAAG 421  
Qy 176 AspSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 195  
Db 422 GACTCCTTACCAGGCTGACTCTGGGGGCCCTCTGCTGTAAAGGGCTCTCTTCAAGGCATC 481  
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysVal 215  
Db 482 ATCTCTCGGGCGGAGGATCATGTGCTGTCCAAAGACCTGTGTGTATACAAAGGTC 541  
Qy 216 CysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229  
Db 542 TGCAAAATATGTGACTGGATCCAGAACCATGAGACACAT 583

RESULT 14  
BG747134  
LOCUS 639 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602704354F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4857733 5', mRNA sequence.

ACCESSION BG747134

VERSION BG747134.1 GI:14057787

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 639)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI710 row: k column: 14  
High quality sequence stop: 638.

Location/Qualifiers  
1. 639

## FEATURES

source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/note="Torgan: Colon; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)";

## ORIGIN

## Alignment Scores:

Pred. No.: 8,25e-76 Length: 639  
Score: 852.00 Matches: 156  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.36% Mismatches: 0  
Query Match: 67.73% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BG747134 (1-639)

Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
Db 168 ATCATCAGGGGTTGAGTGCAGACCTCATCTCCAGGCTTGGCAGGAGCCCTGTTCAG 227  
Qy 21 LysThrArgLeuLeuCysGlyAlaThrIleLeuAlaProArgTrpLeuLeuThrAlaAla 40  
Db 228 AAGACGGGGTACTCTGTGGGGGACGCTCATGCCCCAGATGGCTCTTCAACACAGC 287  
Qy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisLeuGlnLysGluGlu 60  
Db 288 CACTGCTTCAAGCCCGCTCATAGTTTCACTGGGGGAGCAGACACCTCCAGAGAGGAG 347  
Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 348 GGCTGTGAGCAGACCCCGACAGCCACTGAGTCTTCCCTCCCCACCCGCTTCAACACAGC 407  
Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 408 CTCCTCCCAACAAAGACCCGCAATGACATCATGCTGTGAGATGGCATCGCAGTCTCC 467  
Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 468 ATCACTGGGCTGTGGACCCCTTCCCTTCTCCTCAGCTGTGTCACTGTGTGCACAGC 527  
Qy 121 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
Db 528 TGCCTCATTTCCGGCTGGGGGAGCAGCAGCTCCAGCCCGCCAGGTACGCTGCCTCACAC 587  
Qy 141 ArgCysAlaAsnIleThrIleLeuGluHisGlnLysCysGluAsnAlaTyr 157  
Db 588 CGATGCCCAACATCACCATCATTTGAGCACAGAGTGTGAGAACGGCTTAC 638

## RESULT 15

AY410894

LOCUS 556 bp DNA linear GSS 16-DEC-2003

DEFINITION Mus musculus KLK11 gene, VIRTUAL TRANSCRIPT, partial sequence,



ACCESSION	Db
AY410894	365
VERSION	TGCGCCAGTGTTCGGAAAGAGGCAAGGACTCCTCTCAGGGTGACTCTGGAGGGCCCCCTG
KEYWORDS	424
SOURCE	Qy
ORGANISM	187
REFERENCE	187
AUTHORS	425
	207
	485
	227
	545



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 18:52:07 ; Search time 45 Seconds  
(without alignments)

1605.637 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258

Sequence: 1 IIKGPECKPHSQPWOALFE.....GVYTKVKYVDWIOETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organalle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1235.5	98.2	275	4 Q8IXD7	Q8IXD7 homo sapien
2	1062	84.4	249	11 Q3QYN4	Q3QYN4 mus musculus
3	1062	84.4	276	11 Q3QYN3	Q3QYN3 m hippostas
4	883	54.3	260	4 Q8IWE9	Q8IWE9 homo sapien
5	679	54.0	255	4 Q96RQ0	Q96RQ0 homo sapien
6	678	53.9	254	11 Q8CGR4	Q8CGR4 mus musculus
7	671.5	53.4	276	11 Q8CGR6	Q8CGR6 mus musculus
8	630	50.1	251	11 Q9DB08	Q9DB08 mus musculus
9	623.5	49.6	293	11 Q9D140	Q9D140 mus musculus
10	603	47.9	242	11 Q80V54	Q80V54 mus musculus
11	603	47.9	250	11 Q80V54	Q80V54 mus musculus
12	597.5	47.5	234	11 Q9CV76	Q9CV76 mus musculus
13	590	46.9	246	11 Q9ZIR9	Q9ZIR9 mus musculus
14	588	46.7	246	11 Q9QUK9	Q9QUK9 mus musculus
15	587.5	46.7	235	11 Q63274	Q63274 rattus norv
16	587	46.7	246	11 Q9R0T7	Q9R0T7 mus musculus

17	583.5	46.4	239	11 Q63275	Q63275 rattus norv
18	581.5	46.2	261	11 Q9JW70	Q9JW70 mus musculus
19	574.5	45.7	261	6 Q9N1Q1	Q9N1Q1 saguinus oe
20	574.5	45.7	261	6 Q29474	Q29474 canis famil
21	570.5	45.3	242	13 Q7TIR8	Q7TIR8 pangasius n
22	565.5	45.0	242	13 Q7SX90	Q7SX90 brachydano
23	564.5	44.9	269	4 Q8IU55	Q8IU55 homo sapien
24	564	44.8	251	11 Q54854	Q54854 rattus norv
25	562.5	44.7	247	11 Q9CPN7	Q9CPN7 mus musculus
26	560.5	44.6	237	13 Q9I515	Q9I515 fugu rubrip
27	560.5	44.5	244	13 Q8QGW3	Q8QGW3 mus musculus
28	560	44.5	249	11 Q9IWE3	Q9IWE3 anguilla ja
29	558.5	44.4	245	13 Q42160	Q42160 petromyzon
30	557	44.3	248	13 Q7SZT1	Q7SZT1 xenopus lae
31	556.5	44.2	261	11 Q8C232	Q8C232 mus musculus
32	556.5	44.2	263	11 Q9JW71	Q9JW71 mus musculus
33	556	44.2	240	13 Q98TH0	Q98TH0 engraulis j
34	556	44.2	243	13 Q7SZ06	Q7SZ06 xenopus lae
35	556	44.2	246	11 Q88301	Q88301 mus musculus
36	556	44.2	253	11 Q9IY82	Q9IY82 mus musculus
37	555.5	44.2	222	13 Q8AV11	Q8AV11 oncorhynch
38	554.5	44.1	263	11 Q9JW69	Q9JW69 mus musculus
39	554	44.0	262	4 Q86U61	Q86U61 homo sapien
40	552.5	43.9	244	13 Q42159	Q42159 petromyzon
41	552.5	43.9	254	6 Q9XSN6	Q9XSN6 sus scrofa
42	551.5	43.8	286	4 Q86TG8	Q86TG8 homo sapien
43	551	43.8	246	11 Q7TT42	Q7TT42 mus musculus
44	551	43.8	247	11 Q9CPN9	Q9CPN9 mus musculus
45	549.5	43.7	247	13 Q42158	Q42158 petromyzon

#### ALIGNMENTS

RESULT 1

Q8IXD7	Q8IXD7	PRELIMINARY;	PRT;	275 AA.
AC	Q8IXD7;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Variant form hippostasin/KLK11.			
GN	KLK11.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Nakamura T., Mitsui S., Miki T., Yamaguchi N.;			
RT	"Molecular cloning and expression of a variant form of			
RL	hippostasin/KLK11 in prostate.";			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB078780; BAC54105.1; -			
DR	GO; GO:0004263; F:trypsin activity; IEA.			
DR	GO; GO:0004295; F:trypsin activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR009003; Cys_Ser_trypsin.			
DR	InterPro; IPR01254; Peptidase_S1.			
DR	InterPro; IPR001344; Peptidase_S1A.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SMC0020; Tryp_SPC; 1.			
DR	PROSITE; PS50240; TRYPsin DOM; 1.			
DR	PROSITE; PS00134; TRYPsin_HIS; 1.			
DR	PROSITE; PS00135; TRYPsin_SER; 1.			
SC	SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;			

Query Match 98.2%; Score 1235.5; DB 4; Length 275;  
Best Local Similarity 90.2%; Pred. No. 1,1e-122;  
Matches 229; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

1 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L T A A H C L K P - - - - - 45  
 22 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L T A A H C L K P W S L T S P T H V S P D L S 81  
 46 - - - - - R Y I V H L G Q H N L O K E C E C E T R A T E S F P H P G F N N S L P N K D H R N D I M L V K M 95  
 82 S S N Y C L U S H S R Y I V H L G Q H N L O K E C E C E T R A T E S F P H P G F N N S L P N K D H R N D I M L V K M 141  
 96 A S P V S I T W A V R P L T L S R C V T A G T S C L I S G W G T S P Q L R P H T L R C A N I T I I E H Q K C E N 155  
 142 A S P V S I T W A V R P L T L S R C V T A G T S C L I S G W G T S P Q L R P H T L R C A N I T I I E H Q K C E N 201  
 156 A P G N I T D T M V C A S V Q E G K D S C Q D S G G P L V C N S L O G I I S W G D P C A I T R K P G V Y T K V 215  
 202 A P G N I T D T M V C A S V Q E G K D S C Q D S G G P L V C N S L O G I I S W G D P C A I T R K P G V Y T K V 261  
 216 C K Y V D M I Q E T M K N 229  
 262 C K Y V D M I Q E T M K N 275

RESULT 2  
 Q9QYN4 PRELIMINARY; PRT; 249 AA.  
 AC Q9QYN4;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Hippostasin.  
 GN PRS20.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Yamaguchi N., Mitsui S.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Mitsui S., Yamaguchi N.;  
 RL "cDNA cloning of a novel brain serine protease, Hippostasin.";  
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016226; BAA88825.1; -  
 DR HSP; P00763; IDPO.  
 DR MEROPS; S01.257; -  
 DR MG; MG1:1929977; Prs20.  
 DR GO; GO:0005576; C:extracellular; IDA.  
 DR InterPro; IPR009003; Cys Ser trypsin.  
 DR InterPro; IPR001254; Peptidase S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPsin.  
 DR SMART; SMC0020; Tryp\_SPC; 1.  
 DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 SQ SEQUENCE 249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;

Query Match 84.4%; Score 1062; DB 11; Length 249;  
 Best Local Similarity 81.2%; Pred. No. 2.5e-104;  
 Matches 186; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

1 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L T A A H C L K P R Y I V H L G Q H N L O K E E 60  
 21 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L T A A H C L K P R Y I V H L G Q H N L E K T D 80  
 61 G C S Q T R A T E S F P H P G F N N S L P N K D H R N D I M L V K M A S P V S I T W A V R P L T L S R C V T A G T S 120  
 81 G C S Q R R M A T E S F P H P G F N N S L P N K D H R N D I M L V K M S S P V F F T R A V Q P L T L S P H C V A A G T S 140

121 C L I S G W G T S S P Q L R P H T L R C A N I T I I E H Q K C E N A P G N I T D T M V C A S V Q E G K D S C Q G 180  
 141 C L I S G W G T S S P Q L R P H S L R C A N V S I I E H K E K A P G N I T D T M L C A S V R K E G K D S C Q G 200  
 181 D S G G P L V C N S L O G I I S W G D P C A I T R K P G V Y T K V C K Y V D M I Q E T M K N 229  
 201 D S G G P L V C N S L O G I I S W G D P C A V T R K P G V Y T K V C K Y F N W I H E V R N N 249

RESULT 3  
 Q9QYN3 PRELIMINARY; PRT; 276 AA.  
 AC Q9QYN3;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Hippostasin prostate type (Adult male tongue cDNA, RIKEN full-length enriched library, clone:231001508 product:protease, serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert sequence).  
 GN PRS20.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Yamaguchi N., Mitsui S.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Mitsui S., Okui A., Koninami K., Uemura H., Yamaguchi N.;  
 RL "cDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRS20).";  
 RT Biochim. Biophys. Acta 1494:206-210(2000).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RA Adachi J., Azawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shiragawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RT Nature 420:563-573(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RT Nature 409:685-690(2001).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [7]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [8]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=20530913; PubMed=11076961;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto K., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RL CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; AB016227; BAB36955.1; -;  
 DR EMBL; AK009360; BAB26241.2; -;  
 DR EMBL; AK009720; BAB26461.2; -;  
 DR HSP; P00763; 1DPO.  
 DR MEROPS; S01.257; -;  
 DR MGD; MGI:192977; Prss20.  
 DR GO; GO:0005576; C:extracellular; IDA.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query Match 84.4%; Score 1062; DB 11; Length 276;  
 Best Local Similarity 81.2%; Pred. No. 2.8e-104;  
 Matches 186; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPWAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGHNLOKEE 60  
 DB 48 IIKGECKPHSQPWAALFQKTRLLCGATLIAPRWLLTAHCKRPHYVILLGEHNLEKTD 107  
 QY 61 GCEQRTATSPFPHGFNNSLPNKHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTS 120  
 DB 108 GCEQRMATESPPHGFNNSLPNKHNDIMLVKMASPVFFETRAVQPLTLSPHCVAAGTS 167  
 QY 121 CLISGWGTSPPQLRPLHLCANITIIHOKENAYPGNITDTMVCASVOEGKDSQCG 180  
 DB 168 CLISGWGTSPPQLRPLHLCANITIIHOKENAYPGNITDTMVCASVRKGDSCQ 227  
 QY 181 DSGGLVLCNQSLOGIISWGQDPCAITRKPGVYTKVCKYVDWIQEN 229  
 DB 228 DSGGLVLCNQSLOGIISWGQDPCAVTRKPGVYTKVCKYFNMHEVMRN 276

RESULT 4  
 Q8IW69  
 ID Q8IW69 PRELIMINARY; PRT; 260 AA.  
 AC Q8IW69;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC040887; AAH40887.1; -;  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Query Match 54.3%; Score 683; DB 4; Length 260;  
 Best Local Similarity 51.8%; Pred. No. 4.2e-64;  
 Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IIKGECKPHSQPWAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGHNLOKEE 60  
 DB 33 VLGHECPHSQPWAALFQGLLGGVLVGNWVLTAAHCKPKYTVRLGDHSLQNKD 92  
 QY 61 GCEQRTATSPFPHGFNNSLPNKHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTS 120  
 DB 93 GPEQETPVQSIHPHPCVNSS-DVEDHNHDLMLQLRQDASLGSKVKPISLADHCTQPGQK 151  
 QY 121 CLISGWGTSPPQLRPLHLCANITIIHOKENAYPGNITDTMVCASVOEGKDSQCG 180  
 DB 152 CTVSGMGVTSPRENFPDILNCAEVKIFPKKCEDAYPGQITDMVCASGSKGA-DTCQ 210  
 QY 181 DSGGLVLCNQSLOGIISWGQDPCAITRKPGVYTKVCKYVDWIQEN 224  
 DB 211 DSGGLVLCNQSLOGIISWGQDPCGRSDKPGVYTNICRYLDWIKK 254

RESULT 5  
 Q96RQO  
 ID Q96RQO PRELIMINARY; PRT; 255 AA.  
 AC Q96RQO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Prostinoen.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=21226193; PubMed=11327827;  
 RX Takayama T.K., Carter C.A., Deng T.;  
 RT "Activation of prostate-specific antigen precursor (pro-PSA) by  
 RT prostin, a novel human prostatic serine protease identified by  
 RT degenerate PCR.";  
 RL Biochemistry 40:1679-1687(2001).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; AF303046; AAK62813.1; -;  
 DR HSP; P00761; 1AN1.  
 DR MEROPS; S01.081; -;  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.



Db	28	ECVRNSXQWAGLFLYTLQLCAGLINDQWLLTAHCRKPYLWVRLGEHHLWRWEGPEQL	87
QY	66	RTATESFPHGPNNSLPNKHNRNDIMLVKMASPVSIITWAVRPLTSSRCVTAQTSCLIISG	125
Db	88	LLVTDFFPHGPNPNSANDHNDIMLIRLPKRVLTAPVQPLNLTESRPVPGTQCLIFG	147
QY	126	WGSTSSPOLRLPHTLRCA <sup>NI</sup> IEHOKCENAYPGNITDTMVCASVOEGGKDCSGDSGGP	185
Db	148	WGSVSSKLVQVPMTLQCANISILDNKFCRWAYPGHIFKKILCAGLWEGGRSGCQDGGP	207
QY	186	LVCNQSLOGIISWGDP <sup>CAITRKPGVYTKVKYVDWIQETMKN</sup>	229
Db	208	LVEGTLAGIVGFGPEPCSRPRRPAVYTNVFDYLEWIESPMEXN	251
RESULT 9			
ID	Q9D140	PRELIMINARY;	PRT; 293 AA.
AC	Q9D140;		
DT	01-JUN-2001	(TRENBLrel. 17, Created)	
DT	01-JUN-2001	(TRENBLrel. 17, Last sequence update)	
DT	01-OCT-2003	(TRENBLrel. 25, Last annotation update)	
DE	1110030019RIK	protein.	
GN	1110030019RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Embryo;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,		
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
DR	EMBL; AK003996; BAB23113.1; -.		
DR	HSSP; P00763; IDPO.		
DR	MEROPS; S01.017; -.		
DR	MEROPS; S01.418; -.		
DR	MGD; MGI:1915918; 1110030019RIK.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR009003; Cys Ser trypsin.		
DR	InterPro; IPR001254; Peptidase_S1.		
DR	InterPro; IPR001314; Peptidase_S1A.		
DR	Pfam; PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SM00020; Tryp_SPC; 1.		
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.		
KW	Hydrolase; Protease; Serine protease.		
SEQUENCE	293 AA; 31908 MW; ED1F45D8226FE911		CRC64;

QY	123	ISGWGSSPOLRLPHTLRCA <sup>NI</sup> IEHOKCENAYPGNITDTMVCASVOEGGKDCSGDS	182
Db	160	VSGMTTSPQVNPXTLQCANIELRSDDECRQYVPGKITANMLCAGTKEGGKDCSGDS	219
QY	183	GGPLVNCQSLGIIISWGDP <sup>CAITRKPGVYTKVKYVDWIQETMKN</sup>	228
Db	220	GGPLICNGKLYGIISWGDP <sup>FCQGNRPQVYTRVSKYLWIREIIRN</sup>	265
RESULT 8			
ID	Q9DBQ8	PRELIMINARY;	PRT; 251 AA.
AC	Q9DBQ8;		
DT	01-JUN-2001	(TRENBLrel. 17, Created)	
DT	01-JUN-2001	(TRENBLrel. 17, Last sequence update)	
DT	01-OCT-2003	(TRENBLrel. 25, Last annotation update)	
DE	1200016C12RIK	protein.	
GN	1200016C12RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Lung;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,		
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
DR	EMBL; AK004807; BAB23579.1; -.		
DR	HSSP; P00763; IDPO.		
DR	MEROPS; S01.307; -.		
DR	MGD; MGI:1921082; 1200016C12RIK.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR009003; Cys_Ser_trypsin.		
DR	InterPro; IPR001254; Peptidase_S1.		
DR	InterPro; IPR001314; Peptidase_S1A.		
DR	Pfam; PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SM00020; Tryp_SPC; 1.		
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.		
KW	Hydrolase; Protease; Serine protease.		
SEQUENCE	251 AA; 28153 MW; F4D667F8C80C4A23		CRC64;
Query Match			
Best Local Similarity 50.1%; Score 630; DB 11; Length 251;			
Matches 118; Conservative 36; Mismatches 70; Indels 0; Gaps 0;			
QY	6	ECKPHSQPMAALFKTRLLCGATLTA <sup>PRWLLTAHCRKPYLWVRLGEHHLWRWEGGCGQT</sup>	65





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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK009217; BAB26143.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.020; -.
DR MGD; MGI:1916761; 231008B01Rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER
SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Query Match . 47.5%; Score 597.5; DB 11; Length 234;
Best Local Similarity 47.0%; Pred. No. 4.4e-55;
Matches 108; Conservative 39; Mismatches 78; Indels 5; Gaps 4;

QY 1 IIKGFCKPHSQPQAAALPEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGHNLOKEE 60
Db 1 IYNGVECVKNSQWQVGLFHGKYLRCGGVLVDRKWLTAHCLKPRYIVHLGHNLOKEE 67
QY 61 GCEQRTATESPFPHPGNNSLPNKDHNDIMLVKASPVSIITWAVRPLTLSSRCVTAGTS 120
Db 68 WTEQLRHITFTSIHYSQAYQN--HEHDLRLRLNRPILHTRAVRPAVLPSSCVTTGAM 125
QY 121 CLISGWGTSSPOLRPLHTLRCAITIIHKKENAYPGNITDTMVCASVQEGGKDCSQG 180
Db 126 CHVSGWGTINKPWFPPDLQCLNLSVTSNETCRAVFFGRVTENMLCAG-GEAGKDAQQ 184
QY 181 DSGGPLVCNQSLOGIISNGQ-DPCALTRKPGVYTKVCKYVDWIQETMKN 229
Db 185 DSGGPLVCGVLQGLVSGVSGPCGKGIPGVYTKVCKYTDWIRIVIRN 234

RESULT 13
Q921R9

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ID Q921R9 PRELIMINARY; PRT; 246 AA.
AC Q921R9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TRYPSINogen 16
GN TRYGN16 OR TRYPSINGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Rowen L., Hood L.;
RT "Comparison between strains Balb/C and 129 in a region of the mouse T cell receptor beta locus.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RX MEDLINE=21103195; PubMed=11160223;
RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT "Differential transcriptional regulation of individual TCR Vbeta segments before gene rearrangement.";
RL J. Immunol. 166:1771-1780(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF107342; AAC79083.1; -.
DR HSSP; AE000665; AAB69088.1; -.
DR MEROPS; S01.063; -.
DR MGD; MGI:2148749; Trygn16.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 246 AA; 26134 MW; 34E173B18CA2F463 CRC64;

Query Match 46.3%; Score 590; DB 11; Length 246;
Best Local Similarity 49.8%; Pred. No. 2.9e-54;
Matches 114; Conservative 32; Mismatches 77; Indels 6; Gaps 3;

QY 1 IIKGFCKPHSQPQAAALPEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGHNLOKEE 60
Db 24 IVGYTCRENSVPYQVSL-NSGYHFGGSLINDQWVVAHCVKTRIQVRLGHNINVL 82
QY 61 GCEQRTATESPFPHPGNNSLPNKDHNDIMLVKASPVSIITWAVRPLTLSSRCVTAGTS 120
Db 83 GNEQFIDAAKIIKHPNFRKTLN---NDIMLIKLSPPVTLNARVATVALPSSCAPAGTQ 138
QY 121 CLISGWGTSSPOLRPLHTLRCAITIIHKKENAYPGNITDTMVCASVQEGGKDCSQG 180
Db 139 CLISGWGNTLSFGVSPDLQLQCLDALLPOADCAISPGKITGNMVCAGLEGKDCSQG 198
QY 181 DSGGPLVCNQSLOGIISNGQDPCALTRKPGVYTKVCKYVDWIQETMKN 229
Db 199 DSGGPLVCGELQGVISWGVG-CALPDPNGVYTKVCKYVDWIQDTIAAN 246

RESULT 14
Q90UK9
ID Q90UK9 PRELIMINARY; PRT; 246 AA.
AC Q90UK9;

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Qy	114	CVTAGTSLISGWSTSSPQLRPHLTRCANITIIHOKCENAYPGNITDTMVCASVOEG	173
Db	119	BPXVGTCLVSGWSTKPLISELPDDLQCVNIDLLSNEKTEAYRWKVTDLMLCAGLEG	178
Qy	174	GKDSGQDSGGPLVNCNSLOGIISWGQDPCAITRXPGVYTKVCKYVDNIQETMKNN	229
Db	179	GKDACNGDSGGPLICDGLQGLTSWGSVPCEPHNPGIYTKIIFTSWIKVMKEN	234

Search completed: June 22, 2004, 18:56:20  
Job time : 47 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 18:48:16 ; Search time 60 Seconds  
(without alignments)  
1078.390 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IIRGFCECKPHSQPWQALFE.....GYTYKVKYDVTQIETMKN 229

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	3	AAB21325 Human TLS
2	1258	100.0	250	3	AAV99390 Human PRO
3	1258	100.0	250	4	AA666139 Protein o
4	1258	100.0	250	4	AAU12424 Human PRO
5	1258	100.0	250	4	AB504729 Human sec
6	1258	100.0	250	5	AAU83684 Human PRO
7	1258	100.0	250	5	ABG61816 Prostate
8	1258	100.0	250	5	ABB84920 Human PRO
9	1258	100.0	250	5	ABB95526 Human ang
10	1258	100.0	250	6	ABO17868 Novel hum
11	1258	100.0	250	6	ABU80831 Human PRO
12	1258	100.0	250	6	ABO33797 Novel hum
13	1258	100.0	250	6	ABU81122 Human PRO
14	1258	100.0	250	6	ABU56739 Lung canc
15	1258	100.0	250	6	ABU66822 Human PRO
16	1258	100.0	250	6	ABU59903 Novel sec
17	1258	100.0	250	6	ABO25093 Human sec
18	1258	100.0	250	6	ABU82140 Novel hum
19	1258	100.0	250	6	ABU67098 Human sec
20	1258	100.0	250	6	ADA46025 Novel hum
21	1258	100.0	250	6	AD76456 Human PRO
22	1258	100.0	250	6	AD772320 Human PRO
23	1258	100.0	250	6	ADA19106 Human PRO
24	1258	100.0	250	6	ADA61729 Homo sapi
25	1258	100.0	250	6	ADA19514 Novel hum

26	1258	100.0	250	6	ADB28055 Human PRO
27	1258	100.0	250	6	ADA86534 Novel hum
28	1258	100.0	250	6	ADB16098 Human PRO
29	1258	100.0	250	6	ADA47884 Human PRO
30	1258	100.0	250	6	ABO44736 Novel hum
31	1258	100.0	250	6	ABO33632 Novel hum
32	1258	100.0	250	6	ADA67679 Human PRO
33	1258	100.0	250	6	ADB30686 Human PRO
34	1258	100.0	250	6	ADA85982 Novel hum
35	1258	100.0	250	6	ADA97194 Human PRO
36	1258	100.0	250	6	ADA79498 Human PRO
37	1258	100.0	250	6	ADA87637 Novel hum
38	1258	100.0	250	6	ADA16839 Human PRO
39	1258	100.0	250	6	ADA91931 Novel hum
40	1258	100.0	250	6	ADA14994 Human PRO
41	1258	100.0	250	6	ADB18955 Novel hum
42	1258	100.0	250	6	ADA94170 Human PRO
43	1258	100.0	250	6	ADB20066 Novel hum
44	1258	100.0	250	6	ADA13378 Human PRO
45	1258	100.0	250	6	ABO43401 Novel hum

#### ALIGNMENTS

RESULT 1  
AAB21325  
ID AAB21325 standard; protein; 250 AA.  
XX  
AC AAB21325;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human TLSP.  
XX  
KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; TLSP;  
KW trypsin-like serine protease; kallikrein-like protein; serine protease;  
KW cytosolic; cancer; prostate cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2000053776-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-CAN00258.  
XX  
PR 11-MAR-1999; 99US-0124260P.  
PR 01-APR-1999; 99US-0127386P.  
PR 21-JUL-1999; 99US-0144919P.  
XX  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
XX  
PI Yousef GW, Diamandis EP;  
XX  
DR WPI; 2000-587440/55.  
XX  
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L  
PT protein mediated disorders, especially cancer.  
XX  
PS Example 5; Fig 27; 184p; English.  
XX  
CC The present sequence is human trypsin-like serine protease (TLSP), a  
CC member of the serine protease family. Kallikreins and kallikrein-like  
CC proteins are a subgroup of the serine protease enzyme family. They  
CC catalyze the selective cleavage of specific polypeptide precursors to  
CC release peptides with potent biological activity. Nucleic acids encoding  
CC kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-  
CC L6 have been isolated. The proteins are useful in the treatment,  
CC monitoring and diagnosis of cancers, especially prostate cancer. They  
CC can also be used to identify a substance that can associate with or  
CC mediate the biological activity of the proteins. Antibodies can be used  
CC to treat conditions mediated by the kallikrein-like proteins

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XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 1256; DB 3; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.8e-112;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHQPMQALFEKTRLLCGATLLAPRMLTLPAHCLKRYIVHLGQNLQKEE 60
DB 22 IIKGECKPHQPMQALFEKTRLLCGATLLAPRMLTLPAHCLKRYIVHLGQNLQKEE 81
DB 61 GCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKASPVSTIWAVERPLTSSRCVTAGTS 120
DB 82 GCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKASPVSTIWAVERPLTSSRCVTAGTS 141
QY 121 CLISWGSTSSPOLRPLHTLCANITLIEHCKENAVPGNITDVMCASVOEGKDCSCG 180
DB 142 CLISWGSTSSPOLRPLHTLCANITLIEHCKENAVPGNITDVMCASVOEGKDCSCG 201
QY 181 DSGGLVNCQSLQGIISWGDPCAITRKPGYTVKCKYVWICETMKN 229
DB 202 DSGGLVNCQSLQGIISWGDPCAITRKPGYTVKCKYVWICETMKN 250

RESULT 2
AAV99390
ID AAV99390 standard; protein; 250 AA.
XX
AC AAV99390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunodhesion; pharmaceutical; screening.
XX
CS Homo sapiens.
XX
FN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099772P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099815P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 30-SEP-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102687P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103448P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106023P.
PR 27-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106986P.
PR 03-NOV-1998; 98US-0106987P.
PR 03-NOV-1998; 98US-0106989P.
PR 03-NOV-1998; 98US-0106990P.
PR 03-NOV-1998; 98US-0106995P.
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PR 03-NOV-1998; 98US-0106919P.  
 PR 03-NOV-1998; 98US-0106932P.  
 PR 03-NOV-1998; 98US-0106934P.  
 PR 10-NOV-1998; 98US-01072783P.  
 PR 17-NOV-1998; 98US-0108775P.  
 PR 17-NOV-1998; 98US-0108779P.  
 PR 17-NOV-1998; 98US-0108787P.  
 PR 17-NOV-1998; 98US-0108788P.  
 PR 17-NOV-1998; 98US-0108801P.  
 PR 17-NOV-1998; 98US-0108802P.  
 PR 17-NOV-1998; 98US-0108806P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108867P.  
 PR 17-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 XX (GETH ) GENENTECH INC.  
 XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;  
 FI WPI; 2000-237871/20.  
 DR N-PSDB; AAA37072.  
 XX New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 FT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX Claim 12; Fig 102; 773bp; English.  
 XX  
 XX AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AY99340 to AY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention  
 XX  
 XX Sequence 250 AA;  
 SQ  
 Query Match 100.0%; Score 1258; DB 3; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Protein of the invention #51.  
 XX  
 KW Secreted; transmembrane; gene therapy.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078961-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US004342.  
 XX  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,  
 PI Pan Y, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK,  
 PI Williams PM, Wood WT;  
 XX  
 XX WPI; 2001-071395/08.  
 DR  
 XX  
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX  
 XX Claim 1; Fig 102; 787bp; English.  
 XX  
 XX The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 XX  
 XX Sequence 250 AA;  
 SQ  
 Query Match 100.0%; Score 1258; DB 4; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAU12424  
 ID AAU12424 standard; protein: 250 AA.  
 AC  
 XX AAU12424;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO1279 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US032678.  
 XX  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 06-JAN-2000; 2000WO-US000377.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023528.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 XX  
 PA (GENTECH) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W,  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21496.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 other PRO polypeptides, link bioactive molecules to cells expressing PRO

PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
 PT breast, prostate, cervical.  
 XX  
 PS Claim 12; Fig 506; 813pp; English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
 CC polypeptides. The PRO polypeptides are useful to detect other PRO  
 CC polypeptides, to link bioactive molecules to cells expressing PRO  
 CC polypeptides, to modulate biological activities of cells expressing PRO  
 CC polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample. Some  
 CC of the 275 sequences are also useful to stimulate the release of tumour  
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
 CC differentiation of chondrocytes, the proliferation or gene expression in  
 CC pericyte cells, the release of proteoglycans from cartilage, the  
 CC proliferation of inner ear utricular supporting cells or of T-  
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
 CC VIIa. The PRO polypeptides can be used in assays to identify molecules  
 CC involved in binding interactions. The polynucleotides encoding PRO  
 CC polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy  
 CC  
 SQ Sequence 250 AA:  
 Query Match 100.0%; Score 1258; DB 4; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112; Indels 0; Gaps 0;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIKGFECRPHSQPMQALFEKTRLLCGATLLAPRMLTLAACHLPRYIVHGLQNLQKE 60  
 Db 22 IIKGFECRPHSQPMQALFEKTRLLCGATLLAPRMLTLAACHLPRYIVHGLQNLQKE 81  
 QY 61 GCEQRTITSEFPHPGFNSLPNCKDRDILVYKASPVSTTAVRPLTSSRCVYTGTS 120  
 Db 82 GCEQRTITSEFPHPGFNSLPNCKDRDILVYKASPVSTTAVRPLTSSRCVYTGTS 141  
 QY 121 CLISGSGTSSPOLRLPPTLRCAITITIEHCKENAYAGNTIDMVCASVQEGSKDSQCG 180  
 Db 142 CLISGSGTSSPOLRLPPTLRCAITITIEHCKENAYAGNTIDMVCASVQEGSKDSQCG 201  
 QY 181 DSGGPLVGNOSLGGIISWGDPICAITRRKPGYTKVCKYDVIQETMKNN 229  
 Db 202 DSGGPLVGNOSLGGIISWGDPICAITRRKPGYTKVCKYDVIQETMKNN 250  
 RESULT 5  
 ID ABB50479 standard; protein: 250 AA.  
 AC ABB50479;  
 XX  
 DT 07-FEB-2002 (first entry)  
 XX  
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
 XX  
 KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;  
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 KW cytoskeletal; cardiant; vascular; anti-angiogenic; ophthalmological;  
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;  
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;  
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;  
 KW Gaucher's disease; cardiovascular disease; Schmitzer syndrome; chemotaxis;  
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;  
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;  
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KW Parkinson's disease; infectious disease.  
 XX  
 OS Homo sapiens.



XX MO200162891-A2.  
 XX 30-AUG-2001.  
 XX 21-FEB-2001; 2001WO-US005614.  
 XX 24-FEB-2000; 2000US-0184836P.  
 XX 29-MAR-2000; 2000US-0193170P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;  
 XX Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;  
 XX Florence C, Hu J, Li Y, Kyaw H, Fischer C, Ferris AM, Fan P;  
 XX Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z;  
 XX Greene JM;  
 XX WPI; 2001-625724/72.  
 XX N-PSDB; ABA83372.  
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for  
 XX preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease  
 XX and diabetic retinopathy.  
 XX Claim 11; Page 1181-1182; 1533pp; English.  
 XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted  
 XX proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
 XX activities based on the tissues and cells the genes are expressed in.  
 XX Example of these activities include: immunomodulatory; antisclerotic;  
 XX dermatological; immunosuppressive; anti-inflammatory; antitumor;  
 XX anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;  
 XX neuroprotective; neurotrophic; anticonvulsant; antialzheimer's; vascular;  
 XX antiparkinsonian; antidiabetic; and vulnerary. (I) and (II) can be used  
 XX in gene therapy and vaccine production. (I) and (II) can be used in the  
 XX prevention, diagnosis and treatment of immune disorders (e.g. multiple  
 XX sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
 XX (HIV) infections), hyperproliferative disorders (e.g. cancers and  
 XX Gaucher's disease), cardiovascular diseases (e.g. Schmitz syndrome,  
 XX Chaga's cardiomyopathy and coronary arteriosclerosis), angiocenic  
 XX disorders (e.g. corneal graft neovascularisation and diabetic  
 XX retinopathy), neurological disorders (e.g. Huntington's chorea,  
 XX Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
 XX for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to  
 XX ABA83193 and ABB50300 represent sequences used in the exemplification of  
 XX the present invention  
 XX SQ Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 4; Length 250;  
 Best Local Similarity 100.0%; Pired. No. 2,8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIRGFECKPSPQWALFEKTRILCGATLIAPRWILTAHCKPRIVYIHLGQHNIOKE 60  
 Db 22 IIRGFECKPSPQWALFEKTRILCGATLIAPRWILTAHCKPRIVYIHLGQHNIOKE 81  
 QY 61 GCEOTRATSPFPHPGNNSLPKNDHNDIMLVKASPVSTIAVRPLTSSRCVYAGTS 120  
 Db 82 GCEOTRATSPFPHPGNNSLPKNDHNDIMLVKASPVSTIAVRPLTSSRCVYAGTS 141  
 QY 121 CLISGWSSTSPQRLPHTLRCAITITIEHCKENAPGNTITPWCASVQEGKSCCG 180  
 Db 142 CLISGWSSTSPQRLPHTLRCAITITIEHCKENAPGNTITPWCASVQEGKSCCG 201  
 QY 181 DSGGPLVQNSLOGIISWGDDPCATIRKPGVYTRKVCYVWIGETWKN 229  
 Db 202 DSGGPLVQNSLOGIISWGDDPCATIRKPGVYTRKVCYVWIGETWKN 250

RESULT 6  
 AAU83684

ID AAU83684 standard; protein; 250 AA.  
 AC AAU83684;  
 DT 08-MAY-2002 (first entry)  
 DE Human PRO protein, Seq ID No 186.  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW tumour necrosis factor-alpha.  
 OS Homo sapiens.  
 PN MO200208288-A2.  
 XX 31-JAN-2002.  
 XX 29-JUN-2001; 2001WO-US021066.  
 XX 20-JUL-2000; 2000US-0219556P.  
 XX 25-JUL-2000; 2000US-0220585P.  
 XX 25-JUL-2000; 2000US-0220605P.  
 XX 25-JUL-2000; 2000US-0220607P.  
 XX 25-JUL-2000; 2000US-0220624P.  
 XX 25-JUL-2000; 2000US-0220638P.  
 XX 25-JUL-2000; 2000US-0220664P.  
 XX 25-JUL-2000; 2000US-0220666P.  
 XX 26-JUL-2000; 2000US-0220893P.  
 XX 28-JUL-2000; 2000WO-US020710.  
 XX 01-AUG-2000; 2000US-0222425P.  
 XX 22-AUG-2000; 2000US-0227133P.  
 XX 23-AUG-2000; 2000WO-US023522.  
 XX 24-AUG-2000; 2000WO-US023328.  
 XX 10-NOV-2000; 2000WO-US030873.  
 XX 28-NOV-2000; 2000US-0253646P.  
 XX 01-DEC-2000; 2000WO-US032678.  
 XX 20-DEC-2000; 2000US-00747259.  
 XX 20-DEC-2000; 2000WO-US034956.  
 XX 28-FEB-2001; 2001WO-US006520.  
 XX 01-MAR-2001; 2001WO-US006666.  
 XX 22-MAR-2001; 2001US-00816744.  
 XX 10-MAY-2001; 2001US-00854208.  
 XX 10-MAY-2001; 2001US-00854280.  
 XX 25-MAY-2001; 2001WO-US017092.  
 XX (GENTECH ) GENENTECH INC.  
 XX Baker KP, Deenoyers L, Gerritsen ME, Godowski PJ,  
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
 XX WPI; 2002-172001/22.  
 XX N-PSDB; ABR33628.  
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 XX useful for treating a PRO related disorder and for diagnosing tumors such  
 XX as liver tumor, colon cancer, breast tumor, prostate tumor, rectal tumor  
 XX or liver tumor.  
 XX Claim 11; Fig 186; 359pp; English.  
 XX The invention relates to one hundred and twenty two nucleic acids  
 XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 XX encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 XX agonists and antagonists are useful for treating a PRO related disorder.  
 XX The PRO polypeptides are useful for diagnosing tumors, especially lung  
 XX cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
 XX liver tumor. The PRO polypeptides are useful for stimulating the  
 XX proliferation of, or gene expression, in pericyte cells, for stimulating  
 XX the proliferation or differentiation of chondrocyte cells, for  
 XX stimulating the release of tumour necrosis factor-alpha from human blood,  
 XX for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
CC protein sequences of the invention

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 5; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCKLPRTYVHLGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCKLPRTYVHLGQHNLOKEE 81  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSGTSPPQRLPPTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDCSCG 180  
DB 142 CLISGWSGTSPPQRLPPTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDCSCG 201  
QY 181 DSGGFLVNCOSLQGIISWGDPICAITRKPGVYTKVCKYVDWIOETMKN 229  
DB 202 DSGGFLVNCOSLQGIISWGDPICAITRKPGVYTKVCKYVDWIOETMKN 250

## RESULT 7

ABG61816  
ID ABG61816 standard; protein; 250 AA.

XX AC ABG61816;

XX DT 15-AUG-2002 (first entry)

XX DE Prostate cancer-associated protein #17.

XX KM Prostate cancer; prostate tumour tissue; human; mammal; cyrostatic.

XX OS Mammalia.

XX FN WO200230268-A2.

XX PD 18-APR-2002.

XX PF 12-OCT-2001; 2001WO-US032045.

XX PR 13-OCT-2000; 2000US-00687576.

XX PR 08-DEC-2000; 2000US-00733288.

XX PR 08-DEC-2000; 2000US-00733742.

XX PR 24-JAN-2001; 2001US-0263957P.

XX PR 16-MAR-2001; 2001US-0276791P.

XX PR 16-MAR-2001; 2001US-0276888P.

XX PR 06-APR-2001; 2001US-0281922P.

XX PR 24-APR-2001; 2001US-0286214P.

XX PR 30-APR-2001; 2001US-00847046.

XX PR 04-MAY-2001; 2001US-0288589P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PL Gish KC, Mack DH, Wilson KE, Afar D, Hevezi F,

XX DR N-PSDB; ABK92131.

XX XX WPI; 2002-471335/50.

XX XX DR N-PSDB; ABK92131.

XX XX PT Detecting a prostate cancer-associated transcript in a patient,

XX XX PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,

XX XX PT by determining if prostate cancer-associated genes are expressed in a

XX XX PT prostate tissue.

XX XX PS Claim 27; Page 314; 436P; English.

XX The present invention relates to methods of detecting a prostate cancer-  
CC associated transcript in a cell from a patient. The method comprises  
CC contacting a biological sample from the patient with prostate cancer-  
CC associated polynucleotides (designated PC genes) that selectively  
CC hybridise to a sequence that is at least 80% identical to them. The  
CC prostate cancer-associated polynucleotide sequences are differentially  
CC expressed in prostate tumour tissue or in prostate cancer and are derived  
CC from the tissues of various organisms such as humans or other mammals  
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
CC associated genes are useful for diagnosing or treating prostate cancer,  
CC as well as for identifying modulators of prostate cancer or agents that  
CC inhibit prostate cancer. The nucleic acid sequences are particularly  
CC useful in gene therapy, as a vaccine or in antisense applications.

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 5; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCKLPRTYVHLGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCKLPRTYVHLGQHNLOKEE 81  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSGTSPPQRLPPTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDCSCG 180  
DB 142 CLISGWSGTSPPQRLPPTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDCSCG 201  
QY 181 DSGGFLVNCOSLQGIISWGDPICAITRKPGVYTKVCKYVDWIOETMKN 229  
DB 202 DSGGFLVNCOSLQGIISWGDPICAITRKPGVYTKVCKYVDWIOETMKN 250

## RESULT 8

ABB84920  
ID ABB84920 standard; protein; 250 AA.

XX AC ABB84920;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO1279 protein sequence SEQ ID NO:208.

XX KM Human; angiogenesis; cardiant; cyrostatic; antiangiogenic; hypotensive;

XX KM vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX KM age-related macular degeneration; arterial restenosis; angina;

XX KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

XX KM wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX FN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PR 23-JUN-2000; 2000US-0213637P.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 28-JUL-2000; 2000WO-US020710.

XX PR 02-AUG-2000; 2000US-0222695P.

17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00766498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00806869.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gertlesen ME, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
XX WPI; 2002-090516/12.  
DR N-PSDB; ABL88175.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 11; Fig 208; 565bp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endotheial or angiogenic disorder in a mammal, e.g.  
CC atherosclerosis, hypertension, cancer, age-related macular degeneration,  
CC atheroclerosis, hyperension, arterial restenosis, rheumatoid arthritis,  
CC aching, myocardial infarctions, thrombophilicis, lymphangitis, tumor  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The PRO polynucleotides have applications in molecular biology,  
CC including use as hybridisation probes, and in chromosome and gene  
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
CC exemplification of the present invention  
XX  
XX Sequence 250 AA:  
SQ  
Query Match 100.0%; Score 1258; DB 5; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKENAYPNITDTWVCASVQSGKDSGCG 180  
Db 142 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKENAYPNITDTWVCASVQSGKDSGCG 201  
QY 181 DSGGPLVNCOSLOGITISKGDPCATIRKPGVITKVCKYVDIMQETWKN 229  
Db 202 DSGGPLVNCOSLOGITISKGDPCATIRKPGVITKVCKYVDIMQETWKN 250  
RESULT 9  
ABB95526  
ID ABB95526 standard; protein; 250 AA.  
XX  
AC ABB95526;  
XX  
DT 19-JUL-2002 (first entry)  
XX  
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.  
XX  
KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KM cardiac; cytostatic; antiangiogenic; hypotensive; vulnerary;  
XX antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX  
PN WO200208284-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 09-JUL-2001; 2001WO-US021735.  
XX  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00766498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00806869.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
XX  
XX (GETH ) GENENTECH INC.  
XX (BAKE/) BAKER K P.  
XX (FER/) FERRARA N.  
XX (GER/) GERBER H.

PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLMAN K U.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AP, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WJ, Ye W, NPI, 2002-171999/22.  
XX  
XX NPI, 2002-171999/22.  
XX  
XX N-PSDB; ABL95664.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 11, Fig 208; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human CC proteins. These are useful for treating or diagnosing a CC cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention  
XX  
XX Sequence 250 AA;  
SQ  
Query Match 100.0%; Score 1258; DB 5; Length 250;  
Best Local Similarity 100.0%; Pred. No.2.8e-112; Mismatches 0; Gaps 0;  
Matches 229; Conservative 0; Indels 0;  
QY 1 IIKGECKPHSQPMALFEKTRLLCGATLAPRWLLTAACHLKPRYVHLGQHNLOKEE 60  
DB 22 IIKGECKPHSQPMALFEKTRLLCGATLAPRWLLTAACHLKPRYVHLGQHNLOKEE 81  
QY 61 GCEQRTTSEFPFPGFNNSLPKNDHRDILVMKASVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTTSEFPFPGFNNSLPKNDHRDILVMKASVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGSTSSPOLRLPHTLRCAITTIIEHCKENAVPGNITDTMVCASVQEGKDCSQG 180  
DB 142 CLISGSGSTSSPOLRLPHTLRCAITTIIEHCKENAVPGNITDTMVCASVQEGKDCSQG 201  
QY 181 DSGGFLVNOGLGIIISWGDPICATIRPGYTYKCYKCYVMIOETMKN 229  
DB 202 DSGGFLVNOGLGIIISWGDPICATIRPGYTYKCYKCYVMIOETMKN 250  
RESULT 10  
AB017868  
ID AB017868 standard; protein, 250 AA.  
XX  
XX AB017868;  
XX  
XX 26-AUG-2003 (first entry)  
XX  
XX Novel human secreted and transmembrane protein PRO1279.  
XX  
XX Human; secreted and transmembrane protein; PRO; antiinflammatory; antiatherosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release;  
KW

KW tumour; inflammatory disease; organ failure; atherosclerosis;  
KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
KW bioreactor; tissue typing.  
XX  
XX Homo sapiens.  
XX  
XX US2003032156-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 06-MAY-2002; 2002US-00140474.  
XX  
XX 31-MAR-1997; 97WO-US005230.  
XX 12-JUN-1998; 98WO-US012456.  
XX 14-JUL-1998; 98WO-US014552.  
XX 28-AUG-1998; 98WO-US017888.  
XX 10-SEP-1998; 98WO-US018824.  
XX 14-SEP-1998; 98WO-US019093.  
XX 14-SEP-1998; 98WO-US019177.  
XX 16-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
XX 07-OCT-1998; 98WO-US021141.  
XX 29-OCT-1998; 98WO-US022991.  
XX 20-NOV-1998; 98WO-US024855.  
XX 01-DEC-1998; 98WO-US025108.  
XX 05-JAN-1999; 99WO-US000106.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99WO-US005190.  
XX 20-APR-1999; 99WO-US008615.  
XX 14-MAY-1999; 99WO-US012252.  
XX 02-JUN-1999; 99WO-US020111.  
XX 01-SEP-1999; 99WO-US020594.  
XX 08-SEP-1999; 99WO-US020594.  
XX 13-SEP-1999; 99WO-US020944.  
XX 15-SEP-1999; 99WO-US021090.  
XX 15-SEP-1999; 99WO-US021547.  
XX 05-OCT-1999; 99WO-US023089.  
XX 29-NOV-1999; 99WO-US028214.  
XX 30-NOV-1999; 99WO-US028313.  
XX 30-NOV-1999; 99WO-US028409.  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028564.  
XX 02-DEC-1999; 99WO-US028565.  
XX 16-DEC-1999; 99WO-US030951.  
XX 20-DEC-1999; 99WO-US030911.  
XX 20-DEC-1999; 99WO-US030999.  
XX 22-DEC-1999; 99WO-US030720.  
XX 30-DEC-1999; 99WO-US031243.  
XX 30-DEC-1999; 99WO-US031274.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 06-JAN-2000; 2000WO-US000277.  
XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 24-FEB-2000; 2000WO-US004914.  
XX 24-FEB-2000; 2000WO-US005004.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005746.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 10-MAR-2000; 2000WO-US006319.  
XX 15-MAR-2000; 2000WO-US006884.  
XX 20-MAR-2000; 2000WO-US007377.  
XX 21-MAR-2000; 2000WO-US007332.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WMO-US014042.  
 PR 30-MAY-2000; 2000WMO-US014941.  
 PR 02-JUN-2000; 2000WMO-US015264.  
 PR 28-JUL-2000; 2000WMO-US020710.  
 PR 11-AUG-2000; 2000WMO-US022031.  
 PR 23-AUG-2000; 2000WMO-US023522.  
 PR 24-AUG-2000; 2000WMO-US023328.  
 PR 08-NOV-2000; 2000WMO-US030952.  
 PR 10-NOV-2000; 2000WMO-US030873.  
 PR 01-DEC-2000; 2000WMO-US032678.  
 PR 20-DEC-2000; 2000WMO-US0747259.  
 PR 20-DEC-2000; 2000WMO-US034956.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WMO-US006520.  
 PR 01-MAR-2001; 2001WMO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WMO-US017092.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001WMO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WMO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WMO-US020116.  
 PR 29-JUN-2001; 2001WMO-US021066.  
 PR 09-JUL-2001; 2001WMO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 PR XX  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2003-341980/32.  
 DR N-PSDB; ACD24105.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, for treating  
 PT inflammation, organ failure, atherosclerosis, cardiac injury,  
 PT infertility, birth defects, premature aging, acquired immunodeficiency  
 PT syndrome (AIDS), or cancer.  
 XX  
 PS Claim 12; Fig 506; 660pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid (I) comprising, or which  
 CC has 80 % sequence identity to, or the full-length coding sequence of, one  
 CC of 275 nucleotide sequences, and which encodes a corresponding  
 CC polypeptide selected from 275 amino acid sequences, where all sequences  
 CC are given in the specification. The polypeptide encoded by (I) is used to  
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
 CC release of tumor necrosis factor (TNF)-alpha from human blood, modulate  
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
 CC the proliferation or differentiation of cells or gene expression,  
 CC stimulate the release of proteoglycans, stimulate the release of cytokine  
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
 CC to factor VIIa, or detect the presence of tumor in a mammal. The nucleic  
 CC acid and polypeptide encoded by it, are useful for treating inflammatory  
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
 CC birth defects, premature aging, acquired immunodeficiency syndrome

CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
 CC hybridisation probes, in chromosome and gene mapping, and in generating  
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
 CC This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide  
 CC  
 SQ Sequence 250 AA;  
 Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIRGFECRHSQWQALAEKTRLLCGATLIPRMLITAAHLKPRYIVHLGQNIQKEE 60  
 DB 22 IIRGFECRHSQWQALAEKTRLLCGATLIPRMLITAAHLKPRYIVHLGQNIQKEE 81  
 QY 61 GCEQRTATESFPHPGFNNSLPKXDRNDIMLVKASPVSTWAVRPLTLSSRCVTAGTS 120  
 DB 62 GCEQRTATESFPHPGFNNSLPKXDRNDIMLVKASPVSTWAVRPLTLSSRCVTAGTS 141  
 QY 121 CLISGWSTSSPOLRLPHTLRCAITIIIEHCKENAYPGNITDTWCASVQSGKDSGCG 180  
 DB 142 CLISGWSTSSPOLRLPHTLRCAITIIIEHCKENAYPGNITDTWCASVQSGKDSGCG 201  
 QY 181 DSGGPLVCNOSLOGIISWGDPCATRKRGVYTKYCKYVDWIOETMKKN 229  
 DB 202 DSGGPLVCNOSLOGIISWGDPCATRKRGVYTKYCKYVDWIOETMKKN 250  
 RESULT 11  
 ABUS0831  
 ID ABUS0831 standard; protein; 250 AA.  
 XX  
 AC ABUS0831;  
 XX  
 DT 23-JUN-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #93.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036635-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 28-AUG-2002; 2002US-00230163.  
 XX  
 PR 25-JUL-2000; 2000US-0220638P.  
 PR 01-JUN-2001; 2001WMO-US017800.  
 PR 29-JUN-2001; 2001WMO-US021066.  
 PR 09-APR-2002; 2002US-00119480.  
 XX  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,  
 DR WPI; 2003-342045/32.  
 DR N-PSDB; ACA66933.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for the manufacture of a medicament for diagnosing or treating  
 PT tumor.  
 XX  
 PS Claim 11; Fig 186; 314pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO

CC polypeptides and polynucleotides are useful for preparing a medicament  
 CC useful in the diagnosis and treatment of tumors. Anti-PRO antibodies are  
 CC useful in diagnostic assays for PRO, by detecting its expression in  
 CC specific cells, tissues or serum, and for affinity purification of PRO  
 CC from recombinant cell culture or natural sources. AB08793-AB080860  
 CC represent the human PRO polypeptides of the invention. Note: The sequence  
 CC data for this patent was obtained in electronic format directly from the  
 CC USPTO web site at [seqdata.uspto.gov/psipdsidentry.html](http://seqdata.uspto.gov/psipdsidentry.html)  
 XX

SO Sequence 250 AA:

Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRMLITAAHCKPRYIVHGGHNLQKEE 60  
 DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRMLITAAHCKPRYIVHGGHNLQKEE 81  
 QY 61 GCEQRTATSPFPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATSPFPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
 QY 121 CLISGWGSTSSPOLRPHTRCANITIIHOKCENAYPGNITDTMVCASVQEGKDCSCG 180  
 DB 142 CLISGWGSTSSPOLRPHTRCANITIIHOKCENAYPGNITDTMVCASVQEGKDCSCG 201  
 QY 181 DSGGPLVNCNQLGGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNQLGGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 12  
 ABO33797  
 ID ABO33797 standard; protein; 250 AA.

XX ABO33797;

DT 17-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1279.

XX Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;  
 KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;  
 KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;  
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;  
 KW liver tumour; bone disorder; cartilage disorder; sports injury;  
 KW arthritis; wound.

XX Homo sapiens.

XX US2003045687-A1.

XX 06-MAR-2003.

PF 12-AUG-2002; 2002US-00218631.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

PA (GETH ) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

DR WPI; 2003-512315/48.

DR N-PSDB; ACD68685.

PT New genes, and its encoded secreted and transmembrane polypeptides,  
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or  
 PT pericyte proliferation, especially for treating lung tumors, arthritis or

PT wounds in a mammal.  
 XX  
 PS Claim 11; Fig 166; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a  
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of  
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are  
 CC fully defined in the specification; or (b) any of 122 nucleotide  
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the  
 CC specification; or the full length coding sequence of any these 122  
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful  
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are  
 CC particularly useful for detecting tumours (e.g. lung tumour, colon  
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)  
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,  
 CC for stimulating the proliferation or differentiation of chondrocyte  
 CC cells, for stimulating proliferation of pericyte cells, or for modulating  
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or  
 CC polypeptide is also useful for treating tumours or various bone and/or  
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The  
 CC PRO polypeptides are useful in drug screening, particularly as targets  
 CC for therapeutic intervention in these diseases. The PRO polypeptides are  
 CC also useful as molecular weight markers, or for chromosome  
 CC identification. The PRO genes are useful as hybridisation probes, or for  
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may  
 CC also be used in gene therapy, particularly for replacing a defective  
 CC gene. This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide  
 XX  
 SO Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRMLITAAHCKPRYIVHGGHNLQKEE 60  
 DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRMLITAAHCKPRYIVHGGHNLQKEE 81  
 QY 61 GCEQRTATSPFPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATSPFPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
 QY 121 CLISGWGSTSSPOLRPHTRCANITIIHOKCENAYPGNITDTMVCASVQEGKDCSCG 180  
 DB 142 CLISGWGSTSSPOLRPHTRCANITIIHOKCENAYPGNITDTMVCASVQEGKDCSCG 201  
 QY 181 DSGGPLVNCNQLGGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNQLGGIISWGDPICATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 13

AB081122  
 ID AB081122 standard; protein; 250 AA.

XX AB081122;

DT 23-JUN-2003 (first entry)

DE Human PRO polypeptide #253.

XX Human; PRO polypeptide; secreted and transmembrane protein;  
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;  
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;  
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;  
 KW hearing loss; coagulation disorder; stroke; heart attack; candida;  
 KW antidiabetic; anorectic; vulnerable; antiarthritic; osteopathic;  
 KW antineumatic; auditory; cerebroprotective; angiogenic.

XX Homo sapiens.

US2003004311-A1.  
 02-JAN-2003.  
 19-DEC-2001; 2001US-00028072.  
 18-JUN-1997; 97US-0049911P.  
 26-AUG-1997; 97US-0056974P.  
 17-SEP-1997; 97US-0059111P.  
 17-SEP-1997; 97US-0059111P.  
 17-SEP-1997; 97US-0059111P.  
 17-SEP-1997; 97US-0059111P.  
 18-SEP-1997; 97US-0059184P.  
 19-SEP-1997; 97US-0059352P.  
 19-SEP-1997; 97US-0059352P.  
 24-SEP-1997; 97US-0059836P.  
 17-OCT-1997; 97US-0062250P.  
 17-OCT-1997; 97US-0062285P.  
 17-OCT-1997; 97US-0062285P.  
 24-OCT-1997; 97US-0063755P.  
 24-OCT-1997; 97US-0062814P.  
 24-OCT-1997; 97US-0062816P.  
 24-OCT-1997; 97US-0063045P.  
 24-OCT-1997; 97US-0063082P.  
 27-OCT-1997; 97US-0063127P.  
 27-OCT-1997; 97US-0063322P.  
 28-OCT-1997; 97US-0063322P.  
 28-OCT-1997; 97US-0063550P.  
 29-OCT-1997; 97US-0063551P.  
 29-OCT-1997; 97US-0063704P.  
 29-OCT-1997; 97US-0063733P.  
 29-OCT-1997; 97US-0063733P.  
 29-OCT-1997; 97US-0063733P.  
 03-NOV-1997; 97US-0064248P.  
 07-NOV-1997; 97US-0064809P.  
 12-NOV-1997; 97US-0065186P.  
 17-NOV-1997; 97US-0065846P.  
 21-NOV-1997; 97US-0066364P.  
 24-NOV-1997; 97US-0066453P.  
 24-NOV-1997; 97US-0066511P.  
 24-NOV-1997; 97US-0066770P.  
 11-DEC-1997; 97US-0069212P.  
 11-DEC-1997; 97US-0069278P.  
 11-DEC-1997; 97US-0069334P.  
 16-DEC-1997; 97US-0069694P.  
 23-JAN-1998; 98US-0072320P.  
 04-FEB-1998; 98US-0073612P.  
 09-FEB-1998; 98US-0074086P.  
 09-FEB-1998; 98US-0074092P.  
 12-MAR-1998; 98US-0077910P.  
 20-MAR-1998; 98US-0078910P.  
 25-MAR-1998; 98US-0079294P.  
 27-MAR-1998; 98US-0079663P.  
 27-MAR-1998; 98US-0079728P.  
 31-MAR-1998; 98US-0080155P.  
 12-JUN-1998; 98WO-US012456.  
 14-JUL-1998; 98WO-US014552.  
 28-AUG-1998; 98WO-US017888.  
 10-SEP-1998; 98WO-US018824.  
 14-SEP-1998; 98WO-US019093.  
 14-SEP-1998; 98WO-US019094.  
 14-SEP-1998; 98WO-US019177.  
 16-SEP-1998; 98WO-US019330.  
 17-SEP-1998; 98WO-US019437.  
 07-OCT-1998; 98WO-US021141.  
 29-OCT-1998; 98WO-US022991.  
 29-OCT-1998; 98WO-US022992.  
 20-NOV-1998; 98WO-US024855.  
 01-DEC-1998; 98WO-US025108.  
 03-JAN-1999; 99WO-US000106.  
 08-MAR-1999; 99WO-US005028.  
 10-MAR-1999; 99WO-US005190.

20-APR-1999; 99WO-US008615.  
 14-MAY-1999; 99WO-US010733.  
 02-JUN-1999; 99WO-US012252.  
 01-SEP-1999; 99WO-US020111.  
 08-SEP-1999; 99WO-US020594.  
 13-SEP-1999; 99WO-US020944.  
 15-SEP-1999; 99WO-US021090.  
 15-SEP-1999; 99WO-US021547.  
 05-OCT-1999; 99WO-US023089.  
 29-NOV-1999; 99WO-US028214.  
 30-NOV-1999; 99WO-US028313.  
 30-NOV-1999; 99WO-US028409.  
 01-DEC-1999; 99WO-US028301.  
 01-DEC-1999; 99WO-US028634.  
 02-DEC-1999; 99WO-US028551.  
 02-DEC-1999; 99WO-US028564.  
 02-DEC-1999; 99WO-US028565.  
 16-DEC-1999; 99WO-US030095.  
 20-DEC-1999; 99WO-US030911.  
 20-DEC-1999; 99WO-US030999.  
 30-DEC-1999; 99WO-US031243.  
 30-DEC-1999; 99WO-US031274.  
 05-JAN-2000; 2000WO-US000219.  
 06-JAN-2000; 2000WO-US000277.  
 06-JAN-2000; 2000WO-US000376.  
 11-FEB-2000; 2000WO-US003565.  
 18-FEB-2000; 2000WO-US003341.  
 18-FEB-2000; 2000WO-US004342.  
 22-FEB-2000; 2000WO-US004414.  
 24-FEB-2000; 2000WO-US004914.  
 24-FEB-2000; 2000WO-US005004.  
 01-MAR-2000; 2000WO-US005601.  
 02-MAR-2000; 2000WO-US005746.  
 (GENENTECH INC.  
 Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 Gerttisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z,  
 WPI; 2003-352836/33.  
 N-PSDB; ACA67246.  
 New isolated PRO polypeptide useful for treating diabetes, rheumatoid  
 arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or  
 heart attack.  
 Claim 12; Fig 506; 643pp; English.  
 The present invention relates to the isolation of novel human PRO  
 polypeptides, and the polynucleotide sequences encoding them. The PRO  
 polypeptides are secreted and transmembrane proteins. The PRO  
 polypeptides and polynucleotides are useful for preparing a medicament  
 useful in the treatment of diabetes, bone and/or cartilage disorders  
 (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,  
 hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders  
 (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic  
 assays for PRO, by detecting its expression in specific cells, tissues or  
 serum, and for affinity purification of PRO from recombinant cell culture  
 or natural sources. AB08070-AB08114 represent the human PRO  
 polypeptides of the invention. Note: The sequence data for this patent  
 was obtained in electronic format directly from the USPTO web site at  
 seqdata.uspto.gov/psipdidentity.html  
 Sequence 250 AA;  
 Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 IIKGFCKPHSQPQALFEKTRILCGATLIPRLTLTAACLKRPYIVHLGQHNLOKEE 60  
 22 IIKGFCKPHSQPQALFEKTRILCGATLIPRLTLTAACLKRPYIVHLGQHNLOKEE 81

QY 61 GCEOTRTATESPFPHPGNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEOTRTATESPFPHPGNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
 QY 121 CLISGSGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTWVCASVOEGKDSGCG 180  
 DB 142 CLISGSGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTWVCASVOEGKDSGCG 201  
 QY 181 DSGGPLVNCNQLGIIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNQLGIIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 250  
 RESULT 14  
 ABUS6739  
 ID ABUS6739 standard; protein; 250 AA.  
 AC ABUS6739;  
 XX 02-APR-2003 (first entry)  
 DE Lung cancer-associated polypeptide #332.  
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;  
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX Unidentified.  
 OS  
 XX MO20286443-A2.  
 PN  
 PD 31-OCT-2002.  
 XX  
 PF 18-APR-2002; 2002MO-US012476.  
 XX  
 PR 18-APR-2001; 2001US-0284770P.  
 PR 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-034370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Aziz N, Murray R;  
 XX  
 DR WPI: 2003-093161/08.  
 DR N-PSDB; ABX76468.  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX  
 BS Claim 27; Page 443-444; 453pp; English.  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridizes  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the  
 CC invention  
 CC  
 XX Sequence 250 AA:  
 QY  
 DB Query Match 100.0%; Score 1258; DB 6; Length 250;  
 DB Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
 DB Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIRGPECKPHSQPQALFEKTRLLCGATIIAPWLITTAHCKPRYIVHAGHNLOKEE 60  
 DB 22 IIRGPECKPHSQPQALFEKTRLLCGATIIAPWLITTAHCKPRYIVHAGHNLOKEE 81  
 QY 61 GCEOTRTATESPFPHPGNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEOTRTATESPFPHPGNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
 QY 121 CLISGSGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTWVCASVOEGKDSGCG 180  
 DB 142 CLISGSGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTWVCASVOEGKDSGCG 201  
 QY 181 DSGGPLVNCNQLGIIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNQLGIIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 250  
 RESULT 15  
 ABUS6822  
 ID ABUS6822 standard; protein; 250 AA.  
 AC ABUS6822;  
 XX  
 DT 23-MAY-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #253.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036180-A1.  
 PD 20-FEB-2003.  
 XX  
 PF 09-MAY-2002; 2002US-00143114.  
 XX  
 PR 31-MAR-1997; 97WO-US005230.  
 PR 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017868.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 14-SEP-1998; 98WO-US019330.  
 PR 15-SEP-1998; 98WO-US019437.  
 PR 17-SEP-1998; 98WO-US021141.  
 PR 07-OCT-1998; 98WO-US022991.  
 PR 29-OCT-1998; 98WO-US022992.  
 PR 29-OCT-1998; 98WO-US024855.  
 PR 20-NOV-1998; 98WO-US025108.  
 PR 01-DEC-1998; 98WO-US000106.  
 PR 05-JAN-1999; 99WO-US005028.  
 PR 08-MAR-1999; 99WO-US005190.  
 PR 10-MAR-1999; 99WO-US008615.  
 PR 20-APR-1999; 99WO-US010733.  
 PR 14-MAY-1999; 99WO-US012252.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 01-SEP-1999; 99WO-US020111.



PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028213.  
 PR 30-NOV-1999; 99WO-US028499.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030939.  
 PR 22-DEC-1999; 99WO-US030720.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 03-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US000365.  
 PR 18-FEB-2000; 2000WO-US000431.  
 PR 18-FEB-2000; 2000WO-US000432.  
 PR 22-FEB-2000; 2000WO-US000414.  
 PR 24-FEB-2000; 2000WO-US000414.  
 PR 24-FEB-2000; 2000WO-US000504.  
 PR 01-MAR-2000; 2000WO-US000501.  
 PR 02-MAR-2000; 2000WO-US000546.  
 PR 10-MAR-2000; 2000WO-US000541.  
 PR 15-MAR-2000; 2000WO-US000631.  
 PR 20-MAR-2000; 2000WO-US000684.  
 PR 21-MAR-2000; 2000WO-US000737.  
 PR 30-MAR-2000; 2000WO-US000732.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023528.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US047259.  
 PR 20-DEC-2000; 2000WO-US049456.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001US-00872835.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WO-US020116.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.

PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927996.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX  
 PA (GENTH) GENENTECH INC.  
 XX  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,  
 XX  
 DR WPI; 2003-332040/31.  
 DR N-PSDB; ACN03855.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue  
 PT typing, and in chromosome identification.  
 XX  
 XX  
 PS Claim 12; Fig 506; 660pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for for-  
 CC identifying agonists or antagonists. The PRO polypeptides are useful for  
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from  
 CC human blood, for stimulating the proliferation or differentiation of  
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide  
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,  
 CC in chromosome and gene mapping, in the generation of antisense RNA and  
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic  
 CC animals or knockout animals, for the genetic analysis of individuals with  
 CC genetic disorders, and in gene therapy. AB06570-AB06684 represent the  
 CC human PRO polypeptides of the invention. Note: The sequence data for this  
 CC patent was obtained in electronic format directly from the USPTO web site  
 CC at seqdata.uspto.gov/psipsideEntry.html  
 XX  
 SQ Sequence 250 AA;  
 Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIKGFECRKHSPQWALFEKTRILCGATILAPRWLITRAHCKRKYIVHIGCHLQEE 60  
 DB 22 IIKGFECRKHSPQWALFEKTRILCGATILAPRWLITRAHCKRKYIVHIGCHLQEE 81  
 QY 61 GCEQRTATSEFPHPGFNNLSJPNKDRNDIMLVKASPVSLTWAVRPYTLSSRCVTAGTS 120  
 DB 82 GCEQRTATSEFPHPGFNNLSJPNKDRNDIMLVKASPVSLTWAVRPYTLSSRCVTAGTS 141  
 QY 121 CLISMGSTSSPQLPHTLTCANTTIEHOKCEYAVGNITDPMVCAVSVEGGDSCG 180  
 DB 142 CLISMGSTSSPQLPHTLTCANTTIEHOKCEYAVGNITDPMVCAVSVEGGDSCG 201  
 QY 181 DSGGPLVNCNOSLGGIISWGDPICALTRKPGVYTKVCKYVDVIOETMKN 229  
 DB 202 DSGGPLVNCNOSLGGIISWGDPICALTRKPGVYTKVCKYVDVIOETMKN 250

Search completed: June 22, 2004, 18:54:53  
 Job time : 63 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 22, 2004, 18:52:42 ; Search time 20 Seconds

(without alignments)  
1101.393 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Sequence: 1 IIKGFECRPHSQPWQALFE.....GYTVCKYVDVIQETMKNN 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase :  
1: p1r1: \*\*  
2: p1r2: \*\*  
3: p1r3: \*\*  
4: p1r4: \*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684	54.4	260	2	156559
2	605.5	48.1	265	1	KORP
3	600.5	47.7	261	2	A31136
4	595.5	47.3	261	1	NGMSG
5	594	47.2	248	2	S55066
6	591.5	47.0	263	2	S15686
7	591	47.0	246	1	TRRT2
8	588	46.7	238	2	S31779
9	587	46.7	246	1	TRRT1
10	585.5	46.5	261	2	A34079
11	581.5	46.2	259	2	B31136
12	578	45.9	232	1	KOPG
13	577.5	45.9	261	2	A29586
14	577.5	45.9	261	2	A29745
15	577	45.9	231	1	TRPGMR
16	574.5	45.7	261	2	S45303
17	571	45.4	246	2	B25528
18	568	45.2	247	1	TRDG
19	567.5	45.1	259	1	KQRTN
20	565.5	45.0	261	2	A25606
21	564.5	44.9	261	2	A44284
22	564.5	44.9	261	1	KOMS1
23	564	44.8	229	1	TRBGR
24	562	44.7	262	1	KOHU
25	560	44.5	248	2	S55067
26	556.5	44.2	257	2	S33772
27	556.5	44.2	261	2	S01971
28	556	44.2	243	2	A35871
29	556	44.2	247	2	S13813

30	553	44.0	247	2	A27547	trypsin (EC 3.4.21
31	552.5	43.9	231	2	S31778	trypsin (EC 3.4.21
32	552.5	43.9	247	2	S05494	trypsin (EC 3.4.21
33	552	43.9	256	1	NGMSA	7S nerve growth fa
34	551.5	43.8	239	2	A27207	tissue kallikrein
35	551.5	43.8	261	1	A32297	semenogelase (EC 3
36	550	43.7	246	1	TRDGC	trypsin (EC 3.4.21
37	548.5	43.6	259	2	A29746	tissue kallikrein
38	548.5	43.6	261	1	S35711	semenogelase (EC 3
39	548.5	43.6	261	2	A41020	tissue kallikrein
40	548.5	43.6	253	2	A53968	serine proteinase
41	544.5	43.3	242	2	S31775	trypsin (EC 3.4.21
42	544.5	43.3	242	2	S49489	trypsin (EC 3.4.21
43	544.5	43.3	242	2	S31776	trypsin (EC 3.4.21
44	543.5	43.2	261	2	JB0236	tissue kallikrein
45	542.5	43.1	261	1	TRMSVS	tissue kallikrein

## ALIGNMENTS

RESULT 1  
156559  
neutropsin - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
C:Accession: 156559  
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nieh  
U. Neurosci. 15, 5088-5097, 1995  
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease ge  
A:Reference number: 156559; PMID:9534817; PMID:7623137  
A:Accession: 156559  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1260 <RES>  
A:Cross-References: GB:D30785; NID:g1648847; PIDN:BA06451.1; PID:g1020091  
C:Superfamily: trypsin; trypsin homology  
F:33-252/Domain: trypsin homology <TRY>

Query Match 54.4%; Score 684; DB 2; Length 260;  
Best Local Similarity 53.1%; Pred. No. 2.9e+53;  
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IIKGFECRPHSQPWQALFEKTRILCGATLAPRWLTAAICLKPRYVHLGQNLQEE 60  
Db 33 IIEGRECIPIHSPQWQALFQGRRLICGVLVGDRVWLTAAICCKQKXSVRLGDHSLQSRD 92  
QY 61 GGEQRTATSPHPGPNNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120  
Db 93 QPEQIQAQSIQHPCYNSNP-EDHSDIMLRQNSANIGDKYKPVOLANLCPKVGOK 151  
QY 121 CIIISWGSTSPQRLPPTLRANCTTIEHCKCENAVPGNTITDNCASVQEGKDSQGG 180  
Db 152 CIIISWGTVTSPQENFPNTLNCAYKISQNKCEBAYGKITEGVACAG-SSNGADTQGG 210  
QY 181 DSGGLVNCQSLQGIISWGQPCATRRKPGVYTVKVCYVDVIQETMKNN 228  
Db 211 DSGGLVCDGMLQGITWSGSDPCKPEKPGVYTVKICRYTTWIKTMDN 258

## RESULT 2

KORP  
tissue kallikrein (EC 3.4.21.35) precursor - rat  
N/Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein  
C/Species: Rattus norvegicus (Norway rat)  
C>Date: 05-Apr-1983 #sequence\_revision 05-Apr-1983 #text\_change 16-Jun-2000  
C:Accession: A00944; A41429; A25137; U00073; A23863; A33359  
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.  
Proc Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982  
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of  
A:Reference number: A00944; PMID:83117659; PMID:8961406  
A:Accession: A00944  
A:Molecule type: mRNA

A:Residues: 1-265 <SWI>  
A:Experimental source: Pancreatic  
R:Kato, H.; Nakamishi, E.; Enyoji, K.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.  
J. Biochem. 102, 1389-1404, 1987  
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi  
A:Reference number: A41429; MUID:88198057; PMID:3482210  
A:Accession: A41429  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 29-53, 'X', 55-87 <KAT>  
R:Gerald, W.L.; Chao, J.; Chao, L.  
Biochim. Biophys. Acta 866, 1-14, 1986  
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization  
A:Reference number: A25137; MUID:86131678; PMID:3004582  
A:Accession: A25137  
A:Molecule type: mRNA  
A:Residues: 115-265 <GER>  
R:Inoue, H.; Fukui, K.; Miyake, Y.  
J. Biochem. 105, 834-840, 1989  
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed  
A:Reference number: JX0073; MUID:89327211; PMID:2753879  
A:Accession: JX0073  
A:Molecule type: DNA  
A:Residues: 1-265 <INO>  
A:Cross-references: GB:D00448; NID:g220792; PIDN:BA00346.1; PID:g220794  
A:Experimental source: Kidney  
R:Ashley, P.L.; MacDonald, R.J.  
Biochemistry 24, 4512-4520, 1985  
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of  
A:Reference number: A23863; MUID:86051477; PMID:2998455  
A:Accession: A23863  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-265 <ASH>  
A:Cross-references: GB:M11563; NID:g205029; PIDN:AAA41464.1; PID:g205030  
A:Experimental source: submaxillary gland  
R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.  
J. Biol. Chem. 264, 7653-7662, 1989  
A:Title: Organization and expression of the rat kallikrein gene family.  
A:Reference number: A33359; MUID:89214217; PMID:2708383  
A:Accession: A33359  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 5-265 <WIN>  
A:Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:g205007; PIDN:AAA414  
A:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin  
C:Comment: The protein presumably assumes the two-chain form by cleavage between residue  
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release  
C:Genetics:  
A:Insertions: 20/1; 73/2; 169/1; 214/3  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; serine; proteinase; zymogen  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-28/Domain: activation peptide #status predicted <APT>  
F:29-255/Product: tissue kallikrein, pancreatic #status predicted <MPT>  
F:25-255/Domain: trypsin homology <TRY>  
F:35-177, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted  
F:69, 124, 217/Active site: His, Asp, Ser #status predicted

Query Match 48.1%; Score 605.5; DB 1; Length 265;  
Best Local Similarity 45.3%; Pred. No. 2,7e-46;  
Matches 107; Conservative 43; Mismatches 79; Indels 7; Gaps 1;

QY 1 IIKFECKPHSQPQWALFEKTRLLCGATLIAPRMILTAHCKPRYIVHLCQHNIOKEE 60  
DB 29 VVGKYNEMNSQPMQVAVYFGEYLCGVLIDPSWITAAHCATDYYQWLRNMLYDEE 86  
QY 61 GCEQRTATSEFPHPGNNLSL-----PKDHRNDIMLVKASPSITWAVRPLTLSSR 113  
DB 89 PFAOHRIVSQSPFHPGNNODLIMNHTROPDDYNSDMLHLHSQPADINDGVKVIDLPLE 148  
QY 114 CVTAGTSCILSGWSTSSPOLRLPHTLRCAITIIIEHOKENAYPENGITDTWVCASVOEG 173

DB 149 EPKVGSTCLASGWSITPDLGLESDLDQCVNIDLLSNEKVEAHEEVTDLMLCAGHMDG 208  
QY 114 GMDSCGSGGPIVONOSLOGISMGDPCATIKPGYTVCKYVMDICMTKMN 229  
DB 209 GMDTKSGSGGPIVONOSLOGISMGDPCATIKPGYTVCKYVMDICMTKMN 264

RESULT 3  
A31136  
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat  
N:Alternate names: glandular prokallikrein 7, submandibular; proteinase A  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 22-Jun-1999  
C:Accession: A31136; S10698; S10699; D41429; B41429; S09315  
R:Chen, Y.P.; Chao, J.; Chao, L.  
Biochemistry 27, 7189-7196, 1988  
A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.  
A:Reference number: A31136; MUID:89088074; PMID:2849988  
A:Accession: A31136  
A:Molecule type: DNA  
A:Residues: 1-261 <CHR>  
A:Cross-references: GB:M19647; GB:J02837; NID:g204999; PIDN:AAA41461.1; PID:g205000  
R:Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.  
FEBS Lett. 265, 137-140, 1990  
A:Title: Substrate specificity of two kallikrein family gene products isolated from the  
A:Reference number: S10698; MUID:90306305; PMID:2194828  
A:Accession: S10698  
A:Molecule type: protein  
A:Residues: 25-36 <ELM>  
A:Accession: S10699  
A:Molecule type: protein  
A:Residues: 112-139 <BL2>  
R:Kato, H.; Nakamishi, E.; Enyoji, K.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.  
J. Biochem. 102, 1389-1404, 1987  
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi  
A:Reference number: A41429; MUID:88198057; PMID:3482210  
A:Accession: A41429  
A:Molecule type: protein  
A:Residues: 112-133 <KAT>  
A:Accession: B41429  
A:Molecule type: protein  
A:Residues: 25-34, 'D', '36-45', 'S', '47-67', 'X', '69-75 <KA2>  
R:Brady, J.M.; MacDonald, R.J.  
Arch. Biochem. Biophys. 278, 342-349, 1990  
A:Title: The expression of two kallikrein gene family members in the rat kidney.  
A:Reference number: S09315; MUID:90225801; PMID:2183721  
A:Accession: S09315  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 43-45, 'S', '47-114', 'A', '116-261 <BRA>  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine; proteinase  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>  
F:25-253/Domain: trypsin homology <TRY>  
F:65, 120, 213/Active site: His, Asp, Ser #status predicted

Query Match 47.7%; Score 600.5; DB 2; Length 261;  
Best Local Similarity 46.2%; Pred. No. 7.4e-46;  
Matches 109; Conservative 39; Mismatches 81; Indels 7; Gaps 1;

QY 1 IIKFECKPHSQPQWALFEKTRLLCGATLIAPRMILTAHCKPRYIVHLCQHNIOKEE 60  
DB 25 VVGKCKEKNQPMQVAVYFGEYLCGVLIDPSWITAAHCSSNNYQWLRNMLYDEE 84  
QY 61 GCEQRTATSEFPHPGNNLSL-----PKDHRNDIMLVKASPSITWAVRPLTLSSR 113  
DB 85 PFAOHRIVSQSPFHPGNNODLIMNHTROPDDYNSDMLHLHSQPADINDGVKVIDLPLE 144  
QY 114 CVTAGTSCILSGWSTSSPOLRLPHTLRCAITIIIEHOKENAYPENGITDTWVCASVOEG 173  
DB 145 EPKVGSTCLASGWSITPDLGLESDLDQCVNIDLLSNEKIKYKXKVTDLMLCAGHLEG 204



A:Cross-references: EMBL:X17352; NID:g55526; PIDN:CAA35232.1; PID:g55527  
A:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:25-255/Domain: trypsin homology <TRY>  
F:65,121,215/Active site: His, Asp, Ser #status predicted

Query Match 47.0%; Score 591.5; DB 2; Length 263;  
Best Local Similarity 44.5%; Pred. No. 4,7e-45;  
Matches 106; Conservative 44; Mismatches 79; Indels 9; Gaps 2;

QY 1 IIGFECKPHSQPQWQALFEKTRLLCGATILAPRWLTAHCLKPRYIVHLCGHNLOKEE 60  
DB 25 IIGFENCKKSNQPMHVAAYRFAFYQCGVLLDAMVWVLAHCYNDKQVWLGRKRRFEDE 84  
QY 61 GCEQRTATSESPFHPGFNSLPNKH-----RNDIMLVKMAFPSITAVAPLTLSS 112  
DB 85 PSAGHQLSKAIHPHGFMSLNDHPHREDVSDNLMVRLKKEPILTDVYKPIPLT 144  
QY 113 RCTVAGTSCLSIGKSTG-SFQRLPHTLRCAANTIEHOKCENAYPGNTDTMVCASVQ 171  
DB 145 EEPVGSRCILASGMSSTPTEEFYSHDLQCVYLELLSNEVCAKAHTEKTDMLCAGEM 204  
QY 172 EGGDSGCGSGGLVLCVQSLQGIISWGDPICATIRKPGVYTVCKYVDMIOETMKNN 229  
DB 205 DGGKDTVCGSGFLICDGLVLTSGPTTCAFPVFGITKLIETRSWIKQVMANN 262

## RESULT 7

trypsin (EC 3.4.21.4) II precursor - rat

N:Alternate names: trypsinogen II

C:Species: Rattus norvegicus (Norway rat)

C:Date: 05-Apr-1993 #sequence\_revision 30-Sep-1987 #text\_change 18-Jul-1997

A:Accession: A22657; A00949

F:Crack: C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.

J. Biol. Chem. 259, 14255-14264, 1984

A:Title: Structure of two related rat pancreatic trypsin genes.

A:Reference number: A22657; MUID:85054880; PMID:6094547

A:Accession: A22657

A:Molecule type: DNA

A:Residues: 1-246 <CRA>

R:MacDonald, R.J.; Steay, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of

A:Reference number: A00948; MUID:82265624; PMID:6896710

A:Accession: A00949

A:Molecule type: mRNA

A:Residues: 9-246 <MAC>

C:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I mRNA

C:Genetics:

A:Introns: 14/1; 67/2

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-23/Domain: activation peptide #status predicted <APR>

F:24-246/Product: trypsin II #status predicted <ENZY>

F:24-239/Domain: trypsin homology <TRY>

F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted

F:63,107,200/Active site: His, Asp, Ser #status predicted

F:73,77,80,85/Binding site: calcium (Glu, Asn, Val, Gln) #status predicted

Query Match 47.0%; Score 591; DB 1; Length 246;  
Best Local Similarity 49.3%; Pred. No. 4.8e-45;  
Matches 113; Conservative 32; Mismatches 78; Indels 6; Gaps 3;

QY 1 IIGFECKPHSQPQWQALFEKTRLLCGATILAPRWLTAHCLKPRYIVHLCGHNLOKEE 60  
DB 24 IIGFYTCQENSIVYQVSL-NSGVHFCGSLINDQWVSAHCYKSHIQVRLSEHNINYLE 82  
QY 61 GCEQRTATSESPFHPGFNSLPNKHNDIMLVKMAFPSITAVAPLTLSSRCVTAGTS 120  
DB 83 GDEQFINAAKIIHGHPFDRKTLN---NDIMLIKSSPKLNARVATVALPSSCAPAGTQ 138

QY 121 CLISGWSSTSPQLPHTLRCAANTIEHOKCENAYPGNTDTMVCASVOEGKDSGCG 180  
DB 139 CLISGWSSTSPQLPHTLRCAANTIEHOKCENAYPGNTDTMVCASVOEGKDSGCG 198  
QY 181 DSGGFLVNCQSLQGIISWGDPICATIRKPGVYTVCKYVDMIOETMKNN 229  
DB 199 DSGGFLVNCQSLQGIISWGDPICATIRKPGVYTVCKYVDMIOETMKNN 246

## RESULT 8

trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C:Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 22-Jun-1999

A:Accession: S66657; S31779

F:Male: R.; Lorenz, J.B.; Smalac, A.O.; Torrisen, K.R.

Eur. J. Biochem. 232, 677-685, 1995

A:Title: Molecular cloning and characterization of anionic and cationic variants of try

A:Reference number: S66657; MUID:96035908; PMID:7556223

A:Accession: S66657

A:Molecule type: mRNA

A:Residues: 1-238 <MAU>

A:Cross-references: EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase

F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>

F:8-15/Domain: activation peptide #status predicted <APR>

F:16-238/Product: trypsin III #status predicted <MAU>

F:16-231/Domain: trypsin homology <TRY>

F:122-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted

F:55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 46.7%; Score 588; DB 2; Length 238;  
Best Local Similarity 48.0%; Pred. No. 8.6e-45;  
Matches 110; Conservative 35; Mismatches 78; Indels 6; Gaps 4;

QY 1 IIGFECKPHSQPQWQALFEKTRLLCGATILAPRWLTAHCLKPRYIVHLCGHNLOKEE 60  
DB 16 IIGFECKPHSQPQWQALFEKTRLLCGATILAPRWLTAHCLKPRYIVHLCGHNLOKEE 74  
QY 61 GCEQRTATSESPFHPGFNSLPNKHNDIMLVKMAFPSITAVAPLTLSSRCVTAGTS 120  
DB 75 GCEQRTATSESPFHPGFNSLPNKHNDIMLVKMAFPSITAVAPLTLSSRCVTAGTS 130  
QY 121 CLISGWSSTSPQLPHTLRCAANTIEHOKCENAYPGNTDTMVCASVOEGKDSGCG 180  
DB 131 CLISGWSSTSPQLPHTLRCAANTIEHOKCENAYPGNTDTMVCASVOEGKDSGCG 190  
QY 181 DSGGFLVNCQSLQGIISWGDPICATIRKPGVYTVCKYVDMIOETMKNN 229  
DB 191 DSGGFLVNCQSLQGIISWGDPICATIRKPGVYTVCKYVDMIOETMKNN 238

## RESULT 9

trypsin (EC 3.4.21.4) I precursor - rat

N:Alternate names: trypsinogen I

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 24-Sep-1999

A:Accession: B22657

A:Molecule type: DNA

A:Residues: 1-246 <CRA>

A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508

A:Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17

R:MacDonald, R.J.; Steay, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of

A:Reference number: A00948; MUID:82265624; PMID:6896710

A:Accession: A00948  
A:Molecule type: mRNA  
A:Residues: 1-246 <MC>  
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA9518.1; PID:g206508  
C:Genetics:  
A:Introns: 14/1; 67/2; 152/1; 197/3  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:1-23/Domain: activation peptide #status predicted <AP>  
F:24-26/Product: trypsin I #status predicted <ENZ>  
F:24-239/Domain: trypsin I homology <TRY>  
F:30-169/48-66/132-233/139-206/171-185/disulfide bonds: #status predicted  
F:63/107/200/Active site: His, Asp, Ser #status predicted  
F:73/77/80/85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 46.7%; Score 587; DB 1; Length 246;  
Best Local Similarity 48.5%; Pred. No. 1,1e-44;  
Matches 111; Conservative 34; Mismatches 78; Indels 6; Gaps 3;

QY 1 IIKGFECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAACHCKPRYIVHLGQHNLOKEE 60  
Db 24 IIVGYTPEHSVPYQVSL-NSGHFCGSLINDQWVSAHCKYSRIQVALGSHNVLE 82

QY 61 GCEQRTATSEFPHPGFNNSLPNDHRNDIMLVKASPVSIWAVRPLTSSRVTASSR 120  
Db 83 GDEQFVAAKIKHPNYSWTLN---NDIMLIKLSPLVTLNRAVAPVALPSACAPAGTQ 138

QY 121 CLISGMSSTSPQRLPHTLRCAANTTIEHCKENAYPGNTITDTCWASVQEGKDSGCG 180  
Db 139 CLISGMNTLISNGNNNDLLQCVDAPVLSCADCEAAPGBITSMTCVGFLEGGKDSGCG 198

QY 181 DSGGPLVNCNLSGIIISWGQDPCATRRPGVYTRVCKYVMIQETMKN 229  
Db 199 DSGGPLVNCNLSGIIISWGQDPCATRRPGVYTRVCKYVMIQETMKN 246

RESULT 10  
A34079  
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat  
N:Alternate names: kallikrein-related proteinase K8  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change 22-Jun-1999  
C:Accession: A34079; S10700  
R:Brady, J.M.; Wines, D.R.; MacDonald, R.J.  
Biochemistry 28, 5203-5210, 1989  
A:Title: Expression of two kallikrein gene family members in the rat prostate.  
A:Reference number: A34079; MUID:89352606; PMID:2765531  
A:Accession: A34079  
A:Status: Preliminary  
A:Molecule type: DNA; mRNA  
A:Residues: 1-261 <BFA>  
A:Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PID:9  
R:Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.  
FEBS Lett 265, 137-140, 1990  
A:Title: Substrate specificity of two kallikrein family gene products isolated from the  
A:Reference number: S10698; MUID:90306305; PMID:2194829  
A:Accession: S10700  
A:Molecule type: Protein  
A:Residues: 25-43/112-138 <ELM>  
A:Experimental source: submaxillary gland  
A>Note: 125-Lys was also found  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:25-253/Domain: trypsin homology <TRY>  
F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>  
F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>  
F:65/120/213/Active site: His, Asp, Ser #status predicted

Query Match 46.5%; Score 585.5; DB 2; Length 261;  
Best Local Similarity 44.5%; Pred. No. 1.6e-44;  
Matches 105; Conservative 41; Mismatches 83; Indels 7; Gaps 1;

QY 1 IIKGFECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAACHCKPRYIVHLGQHNLOKEE 60  
Db 25 IIGGFNCKRNSQPMQVAAVHFNEPQCGVLLHPSVAVITAAHCYSVNYQVWIGRNNLLADE 84

QY 61 GCEQRTATSEFPHPGFNNSL-----PNDHRNDIMLVKASPVSIWAVRPLTSSR 113  
Db 85 PFAQRLVQSFPHPGFVLDLIIKHTRKAPGNDYSNDLMLHUKTPADITDGVKYIDLPTE 144

QY 114 CVTACTSCLISGMSSTSPQRLPHTLRCAANTTIEHCKENAYPGNTITDTCWASVQEG 173  
Db 145 EKVYSTCLISGMSITLTKNEFPDDLQCVNIIHLSNEKCIKAYNDEVTDVWLCAGEWDG 204

QY 174 GSDSQGSGGPLVNCNLSGIIISWGQDPCATRRPGVYTRVCKYVMIQETMKN 229  
Db 205 GSDSQGSGGPLVNCNLSGIIISWGQDPCATRRPGVYTRVCKYVMIQETMKN 260

RESULT 11  
B31136  
tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat  
N:Alternate names: glandular prokallikrein 3, submandibular  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 22-Jun-1999  
C:Accession: B31136  
R:Chen, Y.P.; Chao, J.; Chao, J.  
Biochemistry 27, 7189-7196, 1988  
A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.  
A:Reference number: A31136; MUID:8908074; PMID:2845988  
A:Accession: B31136  
A:Molecule type: DNA  
A:Residues: 1-259 <CHE>  
A:Cross-references: GB:M19648; GB:J02837; NID:g205002; PIDN:AAA51640.1; PID:g205004  
A>Note: The authors translated the codon GTC for residue 230 as Cys  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-259/Product: tissue prokallikrein 3, submandibular #status predicted <MAT>  
F:25-251/Domain: trypsin homology <TRY>  
F:63/118/211/Active site: His, Asp, Ser #status predicted

Query Match 46.2%; Score 581.5; DB 2; Length 259;  
Best Local Similarity 44.5%; Pred. No. 3.6e-44;  
Matches 105; Conservative 39; Mismatches 83; Indels 9; Gaps 2;

QY 1 IIKGFECRPHSOPWQALFEKTRLLCGATLLAPRWLLTAACHCKPRYIVHLGQHNLOKEE 60  
Db 25 VVGKCKCKNQPMQVAVI--NRYICGVLIDPSVITAAHCYSNHYVLLGRNNLPFDE 82

QY 61 GCEQRTATSEFPHPGFNNSL-----PNDHRNDIMLVKASPVSIWAVRPLTSSR 113  
Db 83 PFAQRLVQSFPHPGFVLDLIIKHTRKAPGNDYSNDLMLHUKTPADITDGVKYIDLPTE 142

QY 114 CVTACTSCLISGMSSTSPQRLPHTLRCAANTTIEHCKENAYPGNTITDTCWASVQEG 173  
Db 143 EKVYSTCLISGMSSTSPQRLPHTLRCAANTTIEHCKENAYPGNTITDTCWASVQEG 202

QY 174 GSDSQGSGGPLVNCNLSGIIISWGQDPCATRRPGVYTRVCKYVMIQETMKN 229  
Db 203 GSDSQGSGGPLVNCNLSGIIISWGQDPCATRRPGVYTRVCKYVMIQETMKN 258

RESULT 12  
K09G  
tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)  
N:Alternate names: glandular kallikrein; kininogenin  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 24-Apr-1984 #sequence\_revision 31-Dec-1993 #text\_change 31-Mar-2000  
C:Accession: A00938; A92895  
R:Hirschschne, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, M.;  
Adv. Exp. Med. Biol. 120, 245-260, 1979  
A:Title: The primary structure of porcine glandular kallikreins.  
A:Reference number: A90015

A:Accession: A00938  
A:Molecule type: protein  
A:Residues: 1-49, 'GMW', 53-134, 'D', 136-156, 'H', 158, 'B', 160-224, 'B', 226-232 <TSC>  
A:Note: the residue identified as 225-Asx is bound to carbohydrate; therefore, we have B  
R:Boyd, W.; Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunik, H.  
J. Mol. Biol. 164, 237-282, 1983  
A:Title: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein A,  
t, structure and its comparison with bovine trypsin.  
A:Reference number: A92895; MUID:83189107; PMID:6551452  
A:Contents: X-ray crystallography, 2 angstroms  
A:Accession: A92895  
A:Molecule type: protein  
A:Residues: 1-224, 'B', 226-232 <BOD>  
A:Comment: The protein consists of two chains, A and B, held together by disulfide bonds  
C:Comment: Tissue kallikrein cleave Met-Iys and Arg-Ser bonds in kininogen to release 1  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: glycoprotein; hydrolase; pancreas; serine proteinase  
F:1-224/Domain: trypsin homology <TRY>  
F:79-82/Region: autocatalysis loop  
F:81-232/Product: tissue kallikrein chain A #status experimental <MP7A>  
F:7-144-26-42-121-190-155-169-180-205/Disulfide bonds: #status experimental  
F:41,89,198/Active site: His, Asp, Ser #status experimental  
F:78/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:225/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 45.9%; Score 578; DB 1; Length 232;  
Best Local Similarity 44.2%; Pred. No. 6,4e-44;  
Matches 102; Conservative 41; Mismatches 86; Indels 2; Gaps 1;

QY 1 IIKGECKPHSQPMQALFEKTRLLCGATLIAPRMILTAHCLKPRYIYHGGHNOKEE 60  
DB 1 IIGRECEKNSHPQVAVIYSSFOCGVILNPKWVLTAAHCNDVYEWLGRHNFENE 60  
QY 61 GCEGTRATSPFPFGNNLSLPKNDIMLVKMASPVITAVRPLTSSRCVAGIS 120  
DB 61 NTQAFEVYADFPHPGNSLADGKDYSHDMLRLQSPATITAVYVLEHPTPEPLGST 120  
QY 121 CLISGWGS--TSSPOLRLPHTLRCAITITIEHCKENAYGNITDTMVCASVOEGKDSG 178  
DB 121 CEASGWSGSIPEGPBFPFDEICQVCLTLQNTFCABAHBKTESLTCAGYLPFGKQDTC 180  
QY 179 QGDSGGLVNCOSLQGISWGQPCATIRKPGVYTVCKXVDIMIOEMKN 229  
DB 181 MGDSGPLICNGKMGQITSMGHTPGCSANKPSITTKLIFYLDWINBITTEN 231

RESULT 13  
A29586  
tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human  
N:Alternate names: glandular kallikrein  
C:Species: Homo sapiens (man)  
C:Date: 08-Mar-1989 #sequence, revision 08-Mar-1989 #text, change 22-Jun-1999  
C:Accession: A29586  
R:Schedlich, L.J.; Bennett, B.H.; Morris, B.J.  
DNA 6, 429-437, 1987  
A:Title: Primary structure of a human glandular kallikrein gene.  
A:Reference number: A29586; MUID:88054467; PMID:2624146  
A:Accession: A29586  
A:Molecule type: DNA  
A:Residues: 1-261 <SCH>  
A:Cross-references: GB:M18157; NID:G186640; PIDN:AAA74454.1; PID:G386842  
A:Note: the authors translated the codon TAC for residue 43 as Trp  
C:Genetics:  
A:Introns: 16/1; 69/2; 165/1; 210/3  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:25-253/Domain: trypsin homology <TRY>  
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 45.9%; Score 577.5; DB 2; Length 261;  
Best Local Similarity 44.9%; Pred. No. 8.1e-44;  
Matches 106; Conservative 42; Mismatches 81; Indels 7; Gaps 1;

QY 1 IIKGECKPHSQPMQALFEKTRLLCGATLIAPRMILTAHCLKPRYIYHGGHNOKEE 60  
DB 25 IIVGMECEKNSHPQVAVIYSSFOCGVILNPKWVLTAAHCNDVYEWLGRHNFENE 84  
QY 61 GCEGTRATSPFPFGNNLSLPKNDIMLVKMASPVITAVRPLTSSRCVAGIS 113  
DB 85 DTGGRVPSHSPFHPVLMVMSLTKQSLRPDESSHDMLRLQSPATITAVYVLEHPT 144  
QY 114 CVTNGTSLISGWGSTSSPOLRLPHTLRCAITITIEHCKENAYGNITDTMVCASVOEG 173  
DB 145 EPALGITVYASGWSGSIPEGPBFPFDEICQVCLTLQNTFCABAHBKTESLTCAGY 204  
QY 174 GKDSCGDSGGLVNCOSLQGISWGQPCATIRKPGVYTVCKXVDIMIOEMKN 229  
DB 205 GKDTCGDSGGLVNCOSLQGISWGQPCATIRKPGVYTVCKXVDIMIOEMKN 260

RESULT 14  
A29745  
tissue kallikrein (EC 3.4.21.35) mGK-9 precursor, submandibular - mouse  
N:Alternate names: glandular kallikrein mGK-9; major epidermal growth factor-binding protein  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1988 #sequence, revision 31-Dec-1988 #text, change 22-Jun-1999  
C:Accession: C29746; A29745; A27120; I70015  
R:Drinkwater, C.C.; Evans, B.A.; Richards, R.I.  
Biochemistry 26, 6750-6756, 1987  
A:Title: Mouse glandular kallikrein genes: identification and characterization of the ge  
A:Reference number: A90522; MUID:88107594; PMID:3322387  
A:Accession: C29746  
A:Molecule type: DNA  
A:Residues: 1-261 <DRI>  
A:Cross-references: GB:M17985; NID:G193476; PIDN:AAA37681.1; PID:G387166  
A:Epidermal source: strain BALB/c, salivary gland  
R:Blaber, M.; Isackson, P.J.; Bradshaw, R.A.  
Biochemistry 26, 6742-6749, 1987  
A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein  
A:Reference number: A29745; MUID:88107593; PMID:3322366  
A:Accession: A29745  
A:Molecule type: mRNA  
A:Residues: 1-261 <BLA>  
A:Cross-references: GB:M17962; NID:G192997; PIDN:AAA37541.1; PID:G309212  
R:Isackson, P.J.; Silverman, R.E.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shooter, E.N.  
Biochemistry 26, 2082-2085, 1987  
A:Title: Epidermal growth factor binding protein: identification of a different protein  
A:Reference number: A27120; MUID:87299636; PMID:3304419  
A:Accession: A27120  
A:Molecule type: protein  
A:Residues: 25-54, 112-124, 'X', 126-130, 165-184, 'X', 186-187, 'X', 189-192 <ISA>  
R:Evans, B.A.; Drinkwater, C.C.; Richards, R.I.  
J. Biol. Chem. 262, 8027-8034, 1987  
A:Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of th  
A:Reference number: I55260; MUID:87250386; PMID:3036794  
A:Accession: I70015  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 70-122 <RBS>  
A:Cross-references: GB:M18608; NID:G198500; PIDN:AAA39351.1; PID:G198506  
A:Comment: This sequence is one of approximately twenty-five members of a gene family or  
C:Genetics:  
A:Gene: KAL  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase; zymogen  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-24/Domain: propeptide #status predicted <PRO>  
F:25-261/Product: tissue kallikrein mGK-9, submandibular #status experimental <MAT>  
F:25-253/Domain: trypsin homology <TRY>  
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 45.9%; Score 577.5; DB 2; Length 261;  
Best Local Similarity 43.2%; Pred. No. 8.1e-44;  
Matches 102; Conservative 48; Mismatches 79; Indels 7; Gaps 1;



```

Qy 1 IIKGECKPSPHMOALAEFKETRLGATLLPMTLLTAADLKRYIVLHGONLKEE 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 25 IVGFEKKEKNSQPMHYAVRYMYEYICGVLIDANWVLRNACHYIENKVSIGKNVLEE 84
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 61 GCEQTRATESPFPGEFNNSL-----PNKRDNDMLVKMAEVSITMAVPELLTSR 113
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 85 PSAQHRVLSKSPFLHPGYNRSLRHNHRIHPEYDYSNDIMLRKSKADITDVVKRIAPTE 144
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 114 CVTAGTSCLLSGMGSSHSPPQLRPHILRCANITIIHQKCEBAYIGNITIDMVCASVQEG 173
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 145 EPKIGSTCVLASGWSGTTPEPKQWANDLQCVNKLKLPNEOCGXAHLEKTDVWLCAGETDG 204
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 174 GSDSCQSDSGAPVNCVSLGGIISMGQDCALITRKPGVYTKCKVDVIOETMANN 229
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 205 GKDTCCKDSGAPLIDCGVLLGITSWQFTTCCGEPKPGVYITLLKTKTSIKTKITMAKN 260
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 15  
PRODUCT

trypsin (EC 3.21.4) precursor - pig (tentative sequence)  
 N:Contains: trypsinogen  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000  
 C:Accession: A90641; A90368; A00947  
 R:Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.  
 Biochim. Biophys. Acta 69, 115-129, 1963  
 A:Title: Su le trypsinogene et la trypsine de porc.  
 A:Reference number: A90641  
 A:Accession: A90641  
 A:Molecule type: Protein  
 A:Residues: 1-10 <CHA>  
 R:Hermosdon, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.  
 Biochemistry 12, 3146-3153, 1973  
 A:Title: Determination of the amino acid sequence of porcine trypsin by sequenator analy  
 A:Reference number: A90368; MUID:73258692; PMID:4738933  
 A:Accession: A90368  
 A:Molecule type: Protein  
 A:Residues: 9-231 <HER>  
 A:Note: at position 20, Ile and Val occur alternately  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; pancreas; polymorphism; Protein digestion; serine proteinase; zym  
 F:1-231/Product: trypsinogen #status experimental <ZYM>  
 F:1-8/Domain: activation peptide #status experimental <APT>  
 F:9-231/Product: trypsin #status experimental <MAT>  
 F:9-224/Domain: trypsin homology <TRY>  
 F:15-145-33-49-117-218-124-191-156-170-181-205/Disulfide bonds: #status predicted  
 F:48-92/186/Active site: His, Asp, Ser #status predicted  
 F:60,62,65,70/Binding site: calcium (Glu, Asp, Val, Glu) #status predicted

Query Match	45.9%;	Score 577;	DB 1;	Length 231;
Best Local Similarity	47.8%;	Prod No. 7	00 44	

Matches 110; Conservative 35; Mismatches 77; Indels 8; Gaps 4;

QY 1 IKGFECRPHSQPQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60

Db 9 IVGGYTCANSIPYQVSLNSGSH-FCGSLINSQWVSAHCHYKSRIQVRLGEHNIDVLE 67

61 GCEQRTATESFPHPGFN-NSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 119

Db 68 GNEQFINAKIITHPNFGNTLD---NDIMLIKSSPATLNSRVATVSLPRSCAAAGT 122

120 SCLISGWGSTSSPQLRPLPHTLRCANITIIHQKCNAYPGNITDTMVCASVQEGKDSQ 179

Dd 123 ECLISGMGNTKSSGSSYPSSLQCLKAPVLSOSSCKSSYPGQITGNMICVGFLEGGKDSQ 182

180 GDSGGPLVCNOSLGGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN 229

Db 183 GDSGGPVVCGQLGIVSWGYG-CAQKNKPGVYTKVCNYYNWIQQTIAAN 231

Search completed: June 22, 2004, 18:56:52  
Job time : 21 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 18:48:51 ; Search time 17 Seconds

(without alignments)  
701.416 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Sequence: 1 IKKFECKPHSGPWQALFE.....GVYTKVCKYVDMIGETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	250	1	KLKB_HUMAN
2	736	58.5	250	1	KLKB_HUMAN
3	687	54.6	250	1	NRPN_RAT
4	684	54.4	250	1	NRPN_MOUSE
5	682	54.2	250	1	KLKB_HUMAN
6	681	54.1	250	1	KLKB_HUMAN
7	677.5	53.9	277	1	KLKB_HUMAN
8	644.5	51.2	293	1	KLKB_HUMAN
9	621	49.4	251	1	KLKB_HUMAN
10	606	48.2	248	1	KLKB_HUMAN
11	605.5	48.1	261	1	KLKB_HUMAN
12	600.5	47.7	261	1	KLKB_HUMAN
13	595.5	47.3	261	1	KLKB_HUMAN
14	594	47.2	248	1	KLKB_HUMAN
15	591.5	47.0	263	1	KLKB_HUMAN
16	591	47.0	246	1	KLKB_HUMAN
17	588	46.7	238	1	KLKB_HUMAN
18	587	46.7	246	1	KLKB_HUMAN
19	585.5	46.5	261	1	KLKB_HUMAN
20	581.5	46.2	259	1	KLKB_HUMAN
21	577.5	45.9	261	1	KLKB_HUMAN
22	577.5	45.9	261	1	KLKB_HUMAN
23	577	45.9	231	1	KLKB_HUMAN
24	577	45.9	244	1	KLKB_HUMAN
25	571	45.4	246	1	KLKB_HUMAN
26	570.5	45.3	246	1	KLKB_HUMAN
27	568	45.2	247	1	KLKB_HUMAN
28	567.5	45.0	259	1	KLKB_HUMAN
29	566.5	44.9	261	1	KLKB_HUMAN
30	564.5	44.9	244	1	KLKB_HUMAN
31	564	44.8	261	1	KLKB_HUMAN
32	564	44.8	243	1	KLKB_HUMAN
33	562	44.7	262	1	KLKB_HUMAN

## ALIGNMENTS

RESULT 1	KLKB_HUMAN	STANDARD	PRT	250 AA.
AC	Q9UBX7; 075837; Q9NS65;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Kalikrein 11 precursor (EC 3.4.21.-) (Hippocastin) (Trypsin-like protease).			
DE	KLK11 OR PRSS20 OR TLSP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Hippocampus;			
RX	MEDLINE=96438738; PubMed=9765601;			
RA	Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiozaki S.;			
RT	cDNA cloning and expression of a novel serine protease, TLSP.			
RL	Biochim. Biophys. Acta 1399:225-228(1998).			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Hippocampus; and Prostate;			
RX	MEDLINE=20329229; PubMed=10872828;			
RA	Mitsui S., Yanada T., Okui A., Komami K., Uemura H., Yamaguchi N.;			
RT	"A novel isoform of a kallikrein-like protease, TLSP/hippocastin,			
RL	Biochem. Biophys. Res. Commun. 272:205-211(2000).			
RN	[3]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20130117; PubMed=10662548;			
RA	Yousef G.M., Scortis A., Diamandis E.P.;			
RT	"Genomic organization, mapping, tissue expression, and hormonal			
RT	regulation of trypsin-like serine protease (TLSP PRSS20), a new			
RL	member of the human kallikrein gene family.";			
RL	Genomics 63:88-96(2000).			
RN	[4]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;			
RT	Moss P., Paepel B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene			
RT	cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[5]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.;			
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.;			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.;			
RA	Dandapani L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.;			
RA	Andrzejewski T., Frankel M., Altix C., Amico-Keller G., Coffield J.;			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.;			
RA	Arellano A., Sanders C., Ow D., Nolan M., Truong S., Kobayashi A.;			
RA	Olsen A.S., Garrano A.V.;			
RT	"Sequence analysis of chromosome 19q13.4.";			

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6] SEQUENCE FROM N.A. (ISOFORM 1).  
 RP TISSUE=Testis;  
 RX MEDLINE=2338257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughall N.A., Peters G.J., Abramson R.D., Mullen S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallat D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Possible multifunctional protease. Efficiently cleaves  
 br-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and  
 CC weakly cleaves other substrates for kallikrein and trypsin.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9UBX7-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9UBX7-2; Sequence=VSP\_005402;  
 CC -1- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform  
 CC 1 is expressed preferentially in brain, isoform 2 in prostate.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 DR EMBL; ABO12917; BA83404.1; ALT\_INIT.  
 DR EMBL; ABO13730; BA88713.1; -  
 DR EMBL; AB041036; BA96797.1; -  
 DR EMBL; AF164623; AA047815.1; -  
 DR EMBL; AF243527; AA933564.1; -  
 DR EMBL; AC011473; AA92357.1; -  
 DR EMBL; BC022068; AA22068.1; -  
 DR HSSP; P00763; IDPO.  
 DR MEROPS; S01.257; -  
 DR Genew; HGNC:6359; KLK11.  
 DR GO; GO:0008236; P:serine-type peptidase activity; TMS.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC\_1.  
 DR PROSITE; PS0240; TRYPSEIN\_DOM\_1.  
 DR PROSITE; PS00134; TRYPSEIN\_HIS\_1.  
 DR PROSITE; PS00135; TRYPSEIN\_SER\_1.  
 KW Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;  
 KM Alternative splicing.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 21 ACTIVATION PEPTIDE (POTENTIAL).  
 FT CHAIN 22 250 KALLIKREIN 11.

FT ACT\_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISTLFD 28 163 BY SIMILARITY.  
 FT DISTLFD 47 63 BY SIMILARITY.  
 FT DISTLFD 135 237 BY SIMILARITY.  
 FT DISTLFD 142 209 BY SIMILARITY.  
 FT DISTLFD 174 188 BY SIMILARITY.  
 FT DISTLFD 199 224 BY SIMILARITY.  
 FT CAROHD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 1 M -> MORELWRMKSNGGLTAAPKPGARSSPLQAM  
 (in isoform 2).  
 FT /Ftd=VSP\_005402.  
 SQ SEQUENCE 250 AA; 2746 MW; 192D910B8C07A56 CRC64;  
 Query Match 100.0%; Score 1258; DB 1; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-109; Mismatches 0; Gaps 0;  
 Matches 229; Conservative 0; Indels 0;  
 QY 1 IIKGECKPHSQPQALFEKTRLLCGATLTAPRWLTAAHCLKPRYIVHLCNLOKKE 60  
 DB 22 IIKGECKPHSQPQALFEKTRLLCGATLTAPRWLTAAHCLKPRYIVHLCNLOKKE 81  
 QY 61 GCEQRTATSEFPHPGFNNSLPNDRNDINLVMAASPVSIWAVRPLTSSRCVTRGTS 120  
 DB 82 GCEQRTATSEFPHPGFNNSLPNDRNDINLVMAASPVSIWAVRPLTSSRCVTRGTS 141  
 QY 121 CLISWGSTSSPOLRPLHTRCANITLIEHOKCNAPVGNITPDMVCAVQEGKDSGCG 180  
 DB 142 CLISWGSTSSPOLRPLHTRCANITLIEHOKCNAPVGNITPDMVCAVQEGKDSGCG 201  
 QY 181 DSGEPLVGNQSLQGIISWGDPICATIRKPGYTVKCYVMIQETMKN 229  
 DB 202 DSGEPLVGNQSLQGIISWGDPICATIRKPGYTVKCYVMIQETMKN 250  
 RESULT 2  
 ID KX9 HUMAN STANDARD; PRT; 250 AA.  
 AC O9UKQ9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-  
 DE L3).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCB Taxid=9606;  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RN MEDLINE=20118156; PubMed=10652563;  
 RN Yousef G.M., Luo L.-Y., Diamandis E.P.;  
 RN "Identification of novel human kallikrein-like genes on chromosome  
 RN 19q13.3-q13.4.";  
 RN Genomics 65:184-194(2000).  
 RN (2)  
 RN SEQUENCE FROM N.A.  
 RN MEDLINE=20247258; PubMed=10783266;  
 RN Yousef G.M., Diamandis E.P.;  
 RN "The expanded human kallikrein gene family: locus characterization and  
 RN molecular cloning of a new member, KLK-L3.";  
 RN Genomics 65:184-194(2000).  
 RN (3)  
 RN SEQUENCE FROM N.A.  
 RN MEDLINE=20510303; PubMed=11054574;  
 RN Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RN Moss P., Paepel B., Wang K.;  
 RN "Sequencing and expression analysis of the serine protease gene



FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 260 AA; 28510 MW, 58DF4F0602A0B7F5 CRC64;  
 Query Match 54.6%; Score 687; DB 1; Length 260;  
 Best Local Similarity 53.5%; Pred. No. 2,7e-56;  
 Matches 121; Conservative 35; Mismatches 68; Indels 2; Gaps 2;

QY 1 IIKGFECKPSPQWQALFEKTRLLCGATLIAPRMILLTAHCHLPRYVILGCHNLOKEE 60  
 33 ILGGECKPSPQWQALFEKTRLLCGATLIAPRMILLTAHCHLPRYVILGCHNLOKEE 92  
 DB 33 ILGGECKPSPQWQALFEKTRLLCGATLIAPRMILLTAHCHLPRYVILGCHNLOKEE 92  
 QY 61 GCEQTRATESPPHGFNNLSFNKDRNDIMLVKASPVSTWAPVPLTSLRCVTAGTS 120  
 DB 93 EPEQEIQVARSIOHPGNSNP-EDHSHDMLIRLONSANLGDKXAPRIELANLCPKVGOK 151  
 QY 121 CLISGWSSTSPQRLPHTLRGANITIEHOKCENAYPGNITPDVWCASVQSGKDCOG 180  
 DB 152 CLISGWSSTSPQRLPHTLRGANITIEHOKCENAYPGNITPDVWCASVQSGKDCOG 210  
 QY 181 DSGGPLYCNCNLSGIIISWGODPCATRKPGVTVKCKYVDWIGETM 226  
 DB 211 DSGGPLYCNCNLSGIIISWGODPCATRKPGVTVKCKYVDWIGETM 256

RESULT 4  
 NRPN MOUSE STANDARD; PRT; 260 AA.  
 ID NRPN MOUSE  
 AC 061955;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Neuropein precursor (EC 3.4.21.-) (NP) (Kallikrein 8).  
 GN K1K8 OR PRSS19 OR NRPN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NBL\_TaxID:10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=Balb/c; TISSUE=Hippocampus;  
 RX MEDLINE=95348817; PubMed=7623137;  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,  
 RA Ito J., Nishino H., Almoco S., Kiyama H., Shiosaka S.;  
 RT "Expression and activity-dependent changes of a novel limbic-serine  
 RT protease gene in the hippocampus."  
 RU J. Neurosci. 15:5088-5097(1995).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RX Yoshida S., Hirata A., Inoue N., Shiosaka S.;  
 RT "Cloning and assignment of mouse neuropein gene, Prss19 to chromosome  
 RT 7B4."  
 RU Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=Czech II; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusha K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldi M.F., Cassavani T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pargue S.J.,  
 RA Rata S.S., Logucliano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren S.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smolius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.T.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RC SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.  
 RC STRAIN=Balb/c; TISSUE=Brain;  
 RX MEDLINE=98225202; PubMed=9556608;  
 RA Shimosaka T., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,  
 RA Shimosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;  
 RT "Characterization of recombinant and brain neuropein, a  
 RT plasticity-related serine protease."  
 RU J. Biol. Chem. 273:11189-11196(1998).  
 RN [5]  
 RC X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.  
 RC TISSUE=Hippocampus;  
 RX MEDLINE=99134351; PubMed=9933620;  
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,  
 RA Shiosaka S., Hakoshima T.;  
 RT "Crystal structure of neuropein, a hippocampal protease involved in  
 RT kindling epileptogenesis."  
 RU J. Biol. Chem. 274:4220-4224(1999).  
 CC -1 FUNCTION: Suggested to be involved in kindling epileptogenesis and  
 CC hippocampal plasticity. Has a strong proteolytic activity against  
 CC fibronectin.  
 CC -1 CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-  
 CC -1 ENZYME REGULATION: Strongly inhibited by diisopropyl  
 CC fluorophosphate, leupeptin and (4-aminophenyl)metanesulfonyl 1-  
 CC fluoride.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 TISSUE SPECIFICITY: Expressed specifically in the limbic system of  
 CC mouse brain and is localized at highest concentration in pyramidal  
 CC neurons of the hippocampal CA1-3 subfields.  
 CC -1 MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260.  
 CC -1 MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.  
 CC -1 SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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 CC -----  
 DR EMBL: D30785; BA06451.1; -  
 DR EMBL: AB032202; BA02435.1; -  
 DR EMBL: BC055895; AA055895.1; -  
 DR PIR: I56559; I56559.  
 DR PDB: INPM; 23-MAR-99.  
 DR MEROPS: S01.244; -  
 DR MGD: MGI:892018; K1x8.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin.1.  
 DR PRINTS: PR00722; CHYOTRYPsin.  
 DR SMART: SM00020; TRYp\_SPC; 1.  
 DR PROSITE: PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyse: Serine protease; Glycoprotein; Zymogen; Signal;  
 KM 3D-structure.  
 FT SIGNAL 1 28  
 FT PROPEP 29 32  
 FT CHAIN 33 260  
 FT ACT\_SITE 73 73  
 FT ACT\_SITE 120 120  
 FT ACT\_SITE 212 212  
 FT DISULFID 39 173  
 FT DISULFID 58 74  
 FT DISULFID 145 246  
 FT DISULFID 152 218  
 FT DISULFID 184 198



FT SIGNAL 1 16 POTENTIAL.  
 FT PROPEP 17 21 ACTIVATION PEPTIDE (POTENTIAL).  
 FT CHAIN 22 256 KALLIKREIN 15.  
 FT ACT\_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 106 106 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 209 209 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPIC 122 206 Missing (in isoform 4).  
 FT VARSPIC 122 256 Missing (in isoform 2).  
 FT VARSPIC 161 161 Missing (in isoform 3).  
 FT VARSPIC 162 256 Missing (in isoform 3).  
 FT VARSPIC 162 256 Missing (in isoform 3).  
 FT CONFLICT 147 160 SHNEPAGSPRSG -> PLSSP (IN REF. 2).  
 FT SEQUENCE 256 AA; 28087 MW; 55EBF8D6022786B5 CRC64;  
 Query Match 54.2%; Score 682; DB 1; Length 256;  
 Best Local Similarity 51.9%; Pred. No. 7.6e-56;  
 Matches 124; Conservative 36; Mismatches 65; Indels 14; Gaps 3;  
 QY 1 IITGFEKPSQPMQALFEKTLTGATLTAFTLTAHCLKRYIVHIGQHNQKE 60  
 DB 22 LLEDECAPHSQPMQVALYERGFPCASLISPHWLSAHCQSRFRVRLGSHNRKD 81  
 QY 61 GCEQTRATSPFPHGFNNSLPKNDHNDIMLVKASPVSIITVAEPLTSSRCVATGS 120  
 DB 82 GPDLRTTSVVIHPRE---ARSHNDIMLVQPAFLNPQVPAVLPTCPHPGEA 137  
 QY 121 CLISGWSGTS-----SP--QLRLPHTLCANITITHEKQENAYFENIDTWCASV 170  
 DB 138 CVVSGMGLVSHNEPRTAGSPRSQVSLPDLTLCANISIIISPTCDKSPRLNTWYCAEA 197  
 QY 171 QEGKSDSCGDSGGLVPCNQLGIIISWGDPCAIRKPKVYKVKYVMIQETMKNN 229  
 DB 198 EGRGABCEGDSGGLVPCNQLGIIISWGDPCAIRKPKVYKVKYVMIQETMKNN 256  
 RESULT 6  
 KLR8 HUMAN STANDARD; PRT; 260 AA.  
 ID KLR8 HUMAN STANDARD; PRT; 260 AA.  
 AC 060259; 09HCB3; Q9UHL3; Q9U047;  
 DT 15-JUN-1999 (Rel. 38, Created)  
 DT 15-JUN-1999 (Rel. 38, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine  
 DE protease TAD3-14) (Tumor-associated differentially expressed gene-14  
 DE protein).  
 GN KLR8 OR PRSS19 OR TAD314 OR NRPN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Hippocampus;  
 RX MEDLINE=98372070; PubMed=9714609;  
 RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;  
 RT "Sequence analysis and expression of human neutropin cDNA and gene.";  
 RL Gene 213:9-16(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=99203457; PubMed=10102990;  
 RA Mitsui S., Tsunokawa N., Yamashiro K., Nakazato H., Yamaguchi N.;  
 RT "A novel form of human neutropin, a brain-related serine protease, is  
 RT generated by alternative splicing and is expressed preferentially in  
 RT human adult brain.";  
 RL Eur. J. Biochem. 260:627-634(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Ovary;  
 RX MEDLINE=99413504; PubMed=10485494;  
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Farley T.H.,  
 RA O'Brien T.J.;  
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel  
 RT serine protease overexpressed by ovarian carcinoma.";  
 RL Cancer Res. 59:4435-4439(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;  
 RT "Molecular cloning and characterization of a novel serine protease,  
 RT ovasin, a potential molecular marker for ovarian carcinoma.";  
 RL Submitted (Sep-1998) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paeger B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [6]  
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,  
 RA Dargatzis L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andrease T., Frankheim M., Altix C., Amico-Keller G., Coefield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan M., Truong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of chromosome 19q13.4".  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases  
 CC - FUNCTION: Suggested to be involved in kindling epileptogenesis and  
 CC hippocampal plasticity.  
 CC - CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=060259-1; Sequence=displayed;  
 CC Name=2;  
 CC IsoId=060259-2; Sequence=VSP\_005401;  
 CC - TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the  
 CC pancreas while isoform 2 is expressed in adult brain and  
 CC hippocampus. Both forms are also found in fetal brain and  
 CC placenta. Not detected in kidney, spleen, liver and lung.  
 CC - SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AB009849; BAA28673.1; -  
 DR EMBL; AB012761; BAA28676.1; -  
 DR EMBL; AB010780; BAA28684.1; -  
 DR EMBL; AB008390; BAA28685.1; -  
 DR EMBL; AB008927; BAA28686.1; -  
 DR EMBL; AF005982; AAD56050.1; -  
 DR EMBL; AF005742; AAD25979.1; -  
 DR EMBL; AF005743; AAD25974.1; -  
 DR EMBL; AF243527; AAG33361.1; -  
 DR EMBL; AC011473; AAG33254.1; -  
 DR HSSP; O61955; INEW.  
 DR MEROPS; S01.244; -  
 DR Genew; HGNC:6369; KLR8.  
 DR MIM; 605644; -  
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.



DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF000089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS00240; TRYP SIN DOM; 1.  
 DR PROSITE: PS00134; TRYP SIN HIS; 1.  
 DR PROSITE: PS00135; TRYP SIN SER; 1.  
 DR Hydrolase: Serine protease; Glycoprotein; Zymogen; Signal;  
 KM Alternative splicing.  
 FT SIGNAL 1 28  
 FT PROPEP 29 32  
 FT CHAIN 33 260  
 FT ACT\_SITE 73 73  
 FT ACT\_SITE 120 120  
 FT ACT\_SITE 212 212  
 FT DISULFID 39 173  
 FT DISULFID 58 74  
 FT DISULFID 145 246  
 FT DISULFID 152 218  
 FT DISULFID 184 198  
 FT DISULFID 208 233  
 FT CARBOHYD 110 110  
 FT VARSPLIC 23 23  
 FT FT  
 FT FT  
 SQ SEQUENCE 260 AA; 28048 MW; EF4395EB8C83E660 CRC64;  
 Query Match 54.1%; Score 681; DB 1; Length 260;  
 Best Local Similarity 51.8%; Pred. No. 9,6e-56;  
 Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;  
 QY 1 IIRGFECKPHSQPQAALEFKTRLLCGATLAPRWLTAAHCKPRYIVHLCQNIQKEE 60  
 DB 33 VLGHEGCPHSPQWQALFQGOOLLGGVLYGVGNWVLTAAHCKPKYTVRLGPHSLQND 92  
 QY 61 GCGOTATATSEFPHPGNNSLPKMDHNDIMVKMASPVSIWAVRPLTSSRCVTAQNS 120  
 DB 93 GPEOELPVVOSIHPHCNNS-DVEDHNDMLQLNDQSLGSKVAPISLADHTOPGCK 151  
 QY 121 CLISGWSSTSPQRLPHILRCANITIIIEHQENAVFPGNITDTWVCASVOEGKSDSCG 180  
 DB 152 CTYSGMGVTSVSPENPFDLTNCAEVKIPQCKCEDAVPGQITDGMVCAQSSKCA-DTCG 210  
 QY 181 DSGGFLVCNOSLOGIISWGDPCALTRKPGVYTKVCKYVDWIOE 224  
 DB 211 DSGGFLVCNOSLOGIISWGDPCALTRKPGVYTKVCKYVDWIOE 254  
 DB  
 RESULT 7  
 KLUKD\_HUMAN STANDARD; PRT; 277 AA.  
 AC Q9UKR3; Q9Y433;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)  
 DE (KLUK-14)  
 GN KLUK13 OR KLUK14.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20223789; PubMed=10766816;  
 RA Yousef G.M., Chang A., Diamandis E.P.,  
 RT "Identification and characterization of KLUK-14, a new kallikrein-like  
 J gene that appears to be down-regulated in breast cancer tissues.";  
 RL J. Biol. Chem. 275:11891-11898(2000).  
 RN  
 RP SEQUENCE FROM N.A.

RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,  
 RA Dandanan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andrieu T., Trankheim M., Attix C., Amico-Keller G., Coffield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carraro A.V.,  
 RT "Sequence analysis of chromosome 19q13.4.";  
 RT Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 RN  
 RP SEQUENCE OF 1-180 FROM N.A.  
 RC TISSUE=uterus;  
 RA Ansoorge W., Warkner U., Mewes H.-W., Gaessenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Secreted (probable).  
 CC -1- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and  
 CC salivary gland.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AF135024; AAD26425.2;  
 CC EMBL: AC014473; AAC23259.1;  
 CC EMBL: AL050220; CAB3320.1; ALT\_INIT.  
 CC HSRP: P00763; IDPO.  
 CC MEROPS: S01.306;  
 CC GeneW: HGNC:6361; KLUK13.  
 CC MIM: 605505;  
 CC GO: GO:0005576; C:extracellular; NAS.  
 CC GO: GO:0004252; F:serine-type endopeptidase activity; NAS.  
 CC GO: GO:0006508; F:proteolysis and peptidolysis; NAS.  
 DR HSRP: P00763; IDPO.  
 DR MEROPS: S01.306;  
 DR GeneW: HGNC:6361; KLUK13.  
 DR MIM: 605505;  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0004252; F:serine-type endopeptidase activity; NAS.  
 DR GO: GO:0006508; F:proteolysis and peptidolysis; NAS.  
 DR InterPro: IPR001254; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001314; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF000089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SMC0020; TRYP\_SPE; 1.  
 DR PROSITE: PS00240; TRYP SIN DOM; 1.  
 DR PROSITE: PS00134; TRYP SIN HIS; 1.  
 DR PROSITE: PS00135; TRYP SIN SER; 1.  
 DR Hydrolase: Serine protease; Glycoprotein; Signal;  
 KW  
 FT SIGNAL 1 16  
 FT CHAIN 17 277  
 FT ACT\_SITE 76 76  
 FT ACT\_SITE 124 124  
 FT ACT\_SITE 218 218  
 FT ACT\_SITE 248 248  
 FT DISULFID 42 178  
 FT DISULFID 61 77  
 FT DISULFID 157 224  
 FT DISULFID 189 203  
 FT DISULFID 214 239  
 FT CARBOHYD 30 30  
 FT CARBOHYD 225 225  
 FT CONFLICT 170 180  
 SQ SEQUENCE 277 AA; 30570 MW; BAA95B8DCFB5D542 CRC64;  
 Query Match 53.9%; Score 677.5; DB 1; Length 277;  
 Best Local Similarity 53.3%; Pred. No. 2.2e-55;  
 Matches 120; Conservative 41; Mismatches 63; Indels 1; Gaps 1;  
 QY 4 GECKPHSQPQWQAALEFKTRLLCGATLAPRWLTAAHCKPRYIVHLCQNIQKEE 63  
 DB 39 GTCPHSPQWQAALEFKTRLLCGATLAPRWLTAAHCKPRYIVHLCQNIQKEE 98  
 QY 64 CRTATSEFPHPGNNSLPKMDHNDIMVKMASPVSIWAVRPLTSSRCVTAQNS 122

Db 99 QVEVHVSIDHPEYRSPHNLNHDHMLLEQSPVQLNGYIOTLPLSHNNRITPCTCR 158  
Qy 123 ISGNGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGKDSQCQS 182  
Db 159 VSGMGTTSPQVNVKPKLQCANIQLSDECRQVYFGKITDMLKAGTEGGKDSCEGDS 218  
Qy 183 GGPVNCQSLQGIISWGDPCCATRRKPGVYTKCKYVDIMQETMK 227  
Db 219 GGPVNCNRLTYGIVSWGDPCCGPPDRPGVYTRVSRVYLMRETR 263

RESULT 8  
KLK5\_HUMAN STANDARD; PRT; 293 AA.  
AC Q9Y37; Q9H8G8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)  
DB (Kallikrein-like protein 2) (KLK-L2).  
GN KLK5 OR SCTE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homindaes; Homo.  
OX NCBI\_Taxid=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Stratum corneum;  
RX MEDLINE=99445563; PubMed=10514489;  
RA Bratseand M., Egelrud T.;  
RT "Purification, molecular cloning, and expression of a human stratum  
RT corneum trypsin-like serine protease with possible function in  
RT desquamation.";  
RL J. Biol. Chem. 274:30033-30040(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20118156; PubMed=10652563;  
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
RT "Identification of novel human kallikrein-like genes on chromosome  
RT 19q13.3-q13.4.";  
RL Anticancer Res. 19:2843-2852(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20510030; PubMed=11054574;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McGuig J.,  
RA Moss P., Paepfer B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene  
RT cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pardee S.J.,  
RA Raba S.S., Loughellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,  
RA Scherch A., Schein U.E., Jones S.U.W., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: May be involved in desquamation.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.  
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
CC  
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DR EMBL: AF168768; AAF03101.1; -  
DR EMBL: AF155028; AAD26429.1; -  
DR EMBL: AF243527; AAG33358.1; -  
DR EMBL: BC008036; AAB08036.1; -  
DR HSRP: P00763; IDPO.  
DR HSRP: S01.017; -  
DR Genew: HGNC:6366; KLK5.  
DR MIM: 605643; -  
DR GO: GO:0005615; C:extracellular space; TAS.  
DR GO: GO:0004252; F:serine-type endopeptidase activity; NAS.  
DR GO: GO:0008544; P:epidermal differentiation; TAS.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro: IPR009003; Cys Ser trypsin.  
DR InterPro: IPR001254; Peptidase S1.  
DR InterPro: IPR001314; Peptidase S1A.  
DR Pfam: PF00089; trypsin. 1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SMO0020; TRY-SPC; 1.  
DR PROSITE: PS02040; TRYPsin DOM; 1.  
DR PROSITE: PS00134; TRYPsin HIS; 1.  
DR PROSITE: PS00135; TRYPsin SER; 1.  
DR Hydrolase; Serine protease; Glycoprotein; Signal.  
KM SIGNAL  
FT CHAIN 1 293  
FT ACT SITE 23 293 KALLIKREIN 5.  
FT ACT SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT SITE 153 153 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT SITE 245 245 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT DISULFID 73 206 BY SIMILARITY.  
FT DISULFID 93 109 BY SIMILARITY.  
FT DISULFID 178 279 BY SIMILARITY.  
FT DISULFID 185 251 BY SIMILARITY.  
FT DISULFID 217 231 BY SIMILARITY.  
FT DISULFID 241 266 BY SIMILARITY.  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 25 56 MISSING (IN REF. 3).  
SQ SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946 CRC64;

Query Match 51.2%; Score 644.5; DB 1; Length 293;  
Best Local Similarity 50.6%; Pred. No. 2.6e-52;  
Matches 117; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

Qy 1 IIKSECKPHSQPQAA-LFEKTELLCGATLIARWILLTAACIKPRYIYHGOHNIQK-58  
Db 67 IINSDDCMHTQPMQALLLRPNQYCGAVLVHPQWLLTAARCKKFRVRLGHYSISPV 126  
Qy 59 EEGCEQRTAIESPHGCFNNSLPNKDRDIMLVKASVSTWMAPELTLSRCCTAG 118  
Db 127 YESQQMFQGVKS-LPHGYS---HPSHSDMLITKRRIRPTKXDRPYNVSHCSAG 182  
Qy 119 TSLISGNGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGKDSQC 178  
Db 183 TKLVISGNGTTSPQVNVKPKLQCANIQLSDECRQVYFGKITDMLKAGTEGGKDSCEGDS 241  
Qy 179 QGDSGGPVNCQSLQGIISWGDPCCATRRKPGVYTKCKYVDIMQETMK 229  
Db 242 QGDSGGPVNCQSLQGIISWGDPCCGPPDRPGVYTRVSRVYLMRETR 292

RESULT 9  
 KLC6 HUMAN STANDARD; PRT; 251 AA.  
 AC Q9P063;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6) (KLC14-16)  
 GN KLC14 OR KLC16.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yousef G.M., Diamandis E.P.;  
 RT "Molecular characterization, mapping, and tissue expression of KLC16, a hormonally regulated kallikrein-like gene."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RA MEDLINE=21250937; PubMed=11352573;  
 RA Hooper U.D., Bul L.T., Rae P.K., Harvey T.J., Myers S.A., Ashworth L.K., Clements J.A.;  
 RT "Identification and characterization of KLC14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."  
 RL Genomics 73:117-122 (2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Lamedin J.E., McCreedy P.M., Skowronski E., Wiswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S., Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gernes J., Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S., Andrade T., Trakheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Avellano A., Sanders C., Ow D., Nolan M., Trong S., Kodayashi A., Olsen A.G., Carraro A.V.;  
 RT "Sequence analysis of chromosome 19q13.4."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP TISSUE SPECIFICITY.  
 RA MEDLINE=20545474; PubMed=10969073;  
 RA Harvey T.J., Hooper U.D., Myers S.A., Stephenson S.A., Ashworth L.K., Clements J.A.;  
 RT "Tissue-specific expression patterns and fine mapping of the human kallikrein (KLC) locus on proximal 19q13.4."  
 RL J. Biol. Chem. 275:37397-37406 (2000).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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 CC  
 DR EMBL, AF161231; AAD50773.2;  
 DR EMBL, AF283669; AAK48523.1;  
 DR EMBL, AF283670; AAK48524.1;  
 DR EMBL, AC011473; AAG23260.1;  
 DR HSSP; P00763; IDPO.  
 DR MEROPS; S01.029;  
 DR Genew; HGNC:6362; KLC14.  
 DR MIM; 606135;  
 GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Signal; Zymogen.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24  
 FT CHAIN 25 251  
 FT ACT\_SITE 67 67 KALLIKREIN 14.  
 FT ACT\_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 31 164 BY SIMILARITY.  
 FT DISULFID 52 68 BY SIMILARITY.  
 FT DISULFID 143 210 BY SIMILARITY.  
 FT DISULFID 175 189 BY SIMILARITY.  
 FT DISULFID 200 225 BY SIMILARITY.  
 SQ SEQUENCE 251 AA; 27452 MW; 9087953BAFAVED25 CRC64;  
 Query Match 49.4%; Score 621; DB 1; Length 251;  
 Best Local Similarity 49.1%; Pred. No. 3.2e-50;  
 Matches 113; Conservative 37; Mismatches 74; Indels 6; Gaps 2;  
 QY 1 IIKPECKPHSPQNALF--EXTRLCATLILAPRWLTAAHCKPRYIVHLGQHLQK 58  
 DB 25 IIGHTCTRSSQPMQALLAAPPRLFCGALLSGQVITAHCGRLPVALAKHNR 84  
 QY 59 EEGCGQTRATESPPHGFNNLSLPKDHRNDITLVKASPVSTIWAYREPLTSSRCTAG 118  
 DB 85 WEATQVAVRVRCVTHPVYN-----SRTHNDIMLOLOQPARISRAVPIEVTOACASFG 140  
 QY 119 TSCLSGSGSTSPQLRPHLTLCANTITIIHOCENAYPPGNTDTWCASVGGKQSC 178  
 DB 141 TSCRVSAGTSSPAPRPAFLQCNINISPEVOCQAYRPTTIPGVCAGVPOGGKQSC 200  
 QY 179 QGDSGGLVPCVQSLGIIISWQDPCALTRKGYVTKYCKYVDMIOETWKN 228  
 DB 201 QGDSGGLVPCVQSLGIIISWQDPCALTRKGYVTKYCKYVDMIOETWKN 250  
 RESULT 10  
 KLC6 HUMAN STANDARD; PRT; 248 AA.  
 AC Q9URF0; Q9URF1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5) (KLC15).  
 GN KLC12 OR KLC15.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA MEDLINE=20118156; PubMed=10652563;  
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
 RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4."  
 RL Anticancer Res. 19:2843-2852 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RA Yousef G.M., Magklara A., Scorillas A., Diamandis E.P.;  
 RT "Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLC15)."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paepker B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region."  
 RL Gene 257:119-130(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,  
 RA Danganan L., Ertler A., Christensen M., Georgescu A., Ayala J., Liu S.,  
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield U.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Aveliano A., Sanders C., Ow D., Nolan M., Truong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of chromosome 19q13.4."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC [1]- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC [1]- ALTERNATIVE PRODUCTS:  
 CC [1]- ALTERNATIVE SPLICING; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9UKR0-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9UKR0-2; Sequence=VSP\_005403;  
 CC [1]- SIMILARITY: Belongs to peptidase family S1. kallikrein subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; AF135025; AAD26426.2; -;  
 DR EMBL; AF135025; AAF06065.1; -;  
 DR EMBL; AF243527; AAG33365.1; -;  
 DR EMBL; AC011473; AAG23258.1; -;  
 DR HSSP; P00763; IDPO.  
 DR MEROPS; S01.020; -;  
 DR Genew; HGNC:6360; KLU12.  
 DR MIM; 605539; -;  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0004552; F:serine-type endopeptidase activity; NAS.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001284; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00240; TRYPsin DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HTS; 1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 KW Hydroxylase; Serine protease; Glycoprotein; Signal;  
 KW Alternative splicing.  
 FT CHAIN 1 17 POTENTIAL.  
 FT ACT\_SITE 18 248 KALLIKREIN 12.  
 FT ACT\_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 28 161 BY SIMILARITY.  
 FT DISULFID 47 63 BY SIMILARITY.  
 FT DISULFID 133 235 BY SIMILARITY.  
 FT DISULFID 140 206 BY SIMILARITY.  
 FT DISULFID 172 186 BY SIMILARITY.  
 FT DISULFID 195 222 BY SIMILARITY.  
 FT CARBOHYD 24 224 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT VARSPIC 236 248 KYDWDIMRMIRNN -> NSTLVGLGTSNMNFCQCP (in

FT isoform 2).  
 FT /FTId=VSP\_005403; CRC64;  
 SQ SEQUENCE 248 AA; 26733 MW; BB473E98F8BAF703 Best Local Similarity 49.6%; Score 606; DB 1; Length 248;  
 Query Match 49.6%; Pred. No. 7,7e-49;  
 Matches 114; Conservative 33; Mismatches 79; Indels 4; Gaps 3;  
 QY 1 IIKGPECKPHSQPQALFFETRLLCATILAPRWLITAAHCLKPRITVHLGCHNLOKEE 60  
 DB 22 IFNTEGGRNSQIPQVGLFBGTSLRCQGVILDHFWVITAAHCGSRWVRLGHSLSQLD 81  
 QY 61 GCEQTPRATESFPFGFNNSLIPNKHNDIMLVMAQSPVITVAVRPLTSSRCVTAGTS 120  
 DB 82 WTEQIRHSGSVTHPTGLGA--STSHEDRLRLRLRPVAVTSSVQPLPLPNCATAGTE 139  
 QY 121 CLISGKSTSPQRLPHTLRCAITITIEHCKENAVPNTITMVCASVQEGKDCSCG 180  
 DB 140 CHVGSGWGTNFRNPFDPDLQLCLMLISVSHATCGVGPGRITSNMCAG--GVGDQACQG 198  
 QY 181 DSGGPLVGNLSGLIISMGQ--DPCAIRKPGVYTKVCKYDWTQETMKN 229  
 DB 199 DSGGPLVCGVQLQVLSMGSYVPGQGDPIFVITVITICKYDWMIRMRNN 248  
 RESULT 11  
 KLU1 RAT STANDARD; PRT; 261 AA.  
 AC P00758.  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) [Tissue  
 DE kallikrein] (PS kallikrein) (RGK-1).  
 GN KLU1 OR KLU-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83117659; PubMed=6961406;  
 RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;  
 RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid  
 RT sequence of the encoded preproenzyme."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Submaxillary gland;  
 RX MEDLINE=86051477; PubMed=2998455;  
 RA Ashley P.L., McDonald R.J.;  
 RT "Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide  
 RT sequences of four distinct types including tonin."  
 RL Biochemistry 24:4512-4520(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=89327211; PubMed=2753879;  
 RA Inoue H., Fukui K., Miyake Y.;  
 RT "Identification and structure of the rat true tissue kallikrein gene  
 RT expressed in the kidney."  
 RL J. Biochem. 105:834-840(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89214217; PubMed=2708383;  
 RA Wines D.R., Brady J.M., Pritchett D.B., Roberts J.L., MacDonald R.J.;  
 RT "Organization and expression of the rat kallikrein gene family."  
 RL J. Biol. Chem. 264:7653-7662(1989).  
 RN [5]  
 RP SEQUENCE OF 48-261 FROM N.A.  
 RX MEDLINE=86131678; PubMed=3004582;  
 RA Gerald W.U., Chao J., Chao L.;  
 RT "Immunological identification of rat tissue kallikrein cDNA and

RT Characterization of the kallikrein gene family.  
 RL Biochim. Biophys. Acta 866:1-14(1986).  
 CC -1- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds  
 CC in kininogen to release Lys-bradykinin.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in  
 CC small molecule substrates. Highly selective action to release  
 CC Kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of  
 CC Met-|-Xaa or Leu-|-Xaa.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J00758; -; NOT ANNOTATED CDS.  
 DR EMBL: M11563; AAA41464.1; ALT\_INIT.  
 DR EMBL: M23876; AAA41462.1; -.  
 DR EMBL: M23874; AAA41462.1; JOINED.  
 DR EMBL: M23875; AAA41462.1; JOINED.  
 DR EMBL: D00448; BAA00346.1; ALT\_INIT.  
 DR EMBL: D00446; BAA00346.1; JOINED.  
 DR EMBL: D00447; BAA00346.1; JOINED.  
 DR EMBL: X03560; CAA27247.1; -.  
 DR PIR: A00944; KORTP.  
 DR HSSP: P00757; ISGF.  
 DR MEROPS: S01.405; -.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin.1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS50240; TRYP\_SIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYP\_SIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYP\_SIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;  
 KW Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24 PROBABLE.  
 FT CHAIN 25 261 ACTIVATION PEPTIDE (PROBABLE).  
 FT CHAIN 1 111 GLANDULAR KALLIKREIN 1.  
 FT CHAIN 2 261  
 FT ACT\_SITE 65 66 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 120 120 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 213 213 CHARGE RELAY SYSTEM.  
 FT DISULFID 31 173 BY SIMILARITY.  
 FT DISULFID 50 66 BY SIMILARITY.  
 FT DISULFID 152 219 BY SIMILARITY.  
 FT DISULFID 184 198 BY SIMILARITY.  
 FT DISULFID 209 234 BY SIMILARITY.  
 FT CARBOHYD 108 108 N-LINKED (GLCNAC...) (PROBABLE).  
 SQ SEQUENCE 261 AA; 28852 MW; F2F9C0227A7882B CRC64;  
 Query Match 48.4%; Score 605.5; DB 1; Length 261;  
 Best Local Similarity 45.3%; Pred. No. 9, 1e-49;  
 Matches 107; Conservative 43; Mismatches 79; Indels 7; Gaps 1;

QY 174 GKDSQGS6GSPVLCVNSLGGIISMGODPCALTRKPGVYTKCYVDMIOETKNN 229  
 DB 205 GKDTCKGDSG6PLICNGVLQGITSGFNPCEPKPGIYTLIKFTPEWIKEMKEN 260  
 RESULT 12  
 ID KAT7\_RAT STANDARD; PRT; 261 AA.  
 AC P36373;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 15-JUN-1994 (Rel. 29, Last sequence update)  
 DE Glandular kallikrein 7, submandibular/renal precursor (EC 3.4.21.35)  
 DE (Tissue kallikrein) (RKG-7) (RSKG-7) (Besterase B) (Proteinase A).  
 GN KUK7 OR KUK-7.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCB:Taxid=10116;  
 RN [1]  
 RP MEDLINE=8908074; PubMed=2849988;  
 RA Chen Y.-P., Chao J., Chao L.;  
 RT "Molecular cloning and characterization of two rat renal kallikrein  
 genes";  
 RL Biochemistry 27:7189-7196(1988).  
 RN [2]  
 RP SEQUENCE OF 25-75.  
 RC TISSUE=Submaxillary gland;  
 RX MEDLINE=88198057; PubMed=3482210;  
 RA Kato H., Nakashishi E., Enjoji K., Hayashi I., Oh-Ishi S., Iwanaga S.;  
 RT "Characterization of serine proteinases isolated from rat  
 submaxillary gland: with special reference to the degradation of rat  
 kininogens by these enzymes";  
 RT J. Biochem. 102:1389-1404(1987).  
 CC -1- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds  
 CC in kininogen to release Lys-bradykinin.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in  
 CC small molecule substrates. Highly selective action to release  
 CC Kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of  
 CC Met-|-Xaa or Leu-|-Xaa.  
 CC -1- TISSUE SPECIFICITY: Kidney and submandibular gland.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
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 CC -----  
 DR EMBL: M19647; AAA41461.1; -.  
 DR PIR: A31136; A31136.  
 DR HSSP: P00759; ITON.  
 DR MEROPS: S01.406; -.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin.1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYP\_SPE; 1.  
 DR PROSITE: PS50240; TRYP\_SIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYP\_SIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYP\_SIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;  
 KW Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24 PROBABLE.  
 FT CHAIN 25 261 GLANDULAR KALLIKREIN 7,  
 FT CHAIN 1 111 SUBMANDIBULAR/RENAL.  
 FT ACT\_SITE 65 65 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 120 120 CHARGE RELAY SYSTEM.

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FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 209 234 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 35 35 S -> D (IN REF. 2).
FT CONFLICT 46 46 T -> S (IN REF. 2).
SQ SEQUENCE 261 AA; 28972 MW; 4PB06C422F25AF16 CRC64;

Query March 47.7%; Score 600.5; DB 1; Length 261;
Best Local Similarity 46.2%; Pred. No. 2; e-48;
Matches 109; Conservative 39; Mismatches 81; Indels 7; Gaps 1;

QY 1 IIKGFECKPHSOPWQALFEKRLTLCATLIAPRMILTAACLPKPYIYHLGQNLQKEE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 25 VIGGYCKEKNQSPQWALYSEFTYXLCQGVLDPSWITTAHGSNNYQWLGNNLLDE 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 GCEOTRATSEFPHGPNNSL-----PKDHRNDIMLVKASPISTMAKPLLSR 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 85 PFAOHRIVSQSPFHPDVKPFLMNRKPKGDHSDMLHLHSOPADITDGVKVDLPTE 144
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 CVAAGTSCISGWSSTSSPOLRLPHLRANITFIHOKENAYPNITDWCASVQEG 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 145 EPRVGSCTLASGWSSTPDLWEPDDLCVNIHLLENKICIKYKREKVTDLWCAGLEEG 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 GKDCSCQDSSGPIVNCNLSGGIISWQDPCATIRKFGVYTKVCKYVDWTOETMKN 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 205 GKDTCTGDSGPIVLCQGVLDPSWITTAHGSNNYQWLGNNLLDE 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
ID KUK3_MOUSE STANDARD; PRT; 261 AA.
AC P00756;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
DE (MGK-3) (7S nerve growth factor gamma chain) (Gamma-NGF).
GN KUK3 OR KUK-3 OR NGFG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85076169; Pubmed=6548955;
RA Ullrich A., Gray A., Wood W.L., Hayflick J., Seeburg P.H.;
RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
RT nerve growth factor using a high-stringency selection procedure.";
RL DNA 3:387-392(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85257431; Pubmed=3848399;
RA Evans B.A., Richards R.I.;
RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
RT are contiguous.";
RL EMBL J. 4:133-138(1985).
RN [3]
RP SEQUENCE OF 25-261.
RX MEDLINE=81264363; Pubmed=7263706;
RA Thomas K.A., Baglan N.C., Bradshaw R.A.;
RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
RT gland 7 S nerve growth factor.";
RL J. Biol. Chem. 256:9156-9166(1981).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
RX STRAIN=Swiss Webster; TISSUE=Submaxillary gland;
RC MEDLINE=98035451; Pubmed=9351801;
RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.Q.;
RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
```

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RT four binding proteins.";
RL Structure 5:1275-1285(1997).
CC -1- FUNCTION: 7S NGF alpha chain stabilizes the 7S complex. The beta
CC dimer promotes neurite growth. The gamma chain is an arginine-
CC specific protease; it may also have plasminogen activator
CC activity as well as mitogenic activity for chick embryo
CC fibroblasts.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallikrein (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-Xaa or Leu-Xaa.
CC -1- COFACTOR: Binds 2 zinc ions per 7S complex. The zinc ions are
CC bound at the alpha-gamma interfaces.
CC -1- SUBUNIT: 7S nerve growth factor is composed of two alpha chains,
CC a beta dimer composed of identical chains, and two gamma chains.
CC -1- MISCELLANEOUS: This precursor is cleaved into segments to produce
CC the active form of the gamma chain, which occurs naturally as
CC combinations of either two or three segments held together by
CC disulfide bonds: B1 and A, or B1, C and B2.
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC -----
DR EMBL; X01389; CAA25645.1; -
DR EMBL; X01798; CAA25928.1; -
DR EMBL; X01799; CAA25930.1; -
DR PIR; A91005; NGMSG.
DR PDB; 1SGF; 27-MAY-98.
DR MEROPS; S01.170; -.
DR MGDI; WGI:97322; NGIS.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSEC; 1.
DR PROSITE; PS50240; TRYPSEC; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KX Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Metal-Binding; Zinc; Signal; Growth factor; 3D-structure;
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 261
FT CHAIN 25 107
FT CHAIN 112 261
FT ACT_SITE 65 65
FT ACT_SITE 120 120
FT ACT_SITE 213 213
FT METAL 231 231
FT METAL 236 236
FT DISULFID 31 173
FT DISULFID 50 66
FT DISULFID 152 219
FT DISULFID 184 198
FT DISULFID 209 234
FT CARBOHYD 102 102
FT CARBOHYD 107 107
FT DOVAIN 112 261
FT DOVAIN 112 261
FT DOVAIN 165 261
FT CONFLICT 108 111
FT STRAND 26 26
FT STRAND 29 30
FT HELIX 33 35
FT TURN 37 38
FT STRAND 39 44
N-LINKED (GLCNAC. . .).
SEGMENT B1.
SEGMENT A.
SEGMENT C.
SEGMENT B2.
MISSING (IN REF. 2).
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FT TURN 45 46  
 FT STRAND 47 46  
 FT TURN 57 58  
 FT STRAND 59 62  
 FT HELIX 64 66  
 FT STRAND 72 75  
 FT STRAND 79 79  
 FT TURN 80 81  
 FT TURN 85 86  
 FT STRAND 88 97  
 FT TURN 99 100  
 FT HELIX 103 105  
 FT TURN 118 119  
 FT STRAND 122 126  
 FT TURN 148 149  
 FT STRAND 151 156  
 FT STRAND 159 159  
 FT STRAND 167 167  
 FT STRAND 170 170  
 FT STRAND 172 179  
 FT HELIX 181 187  
 FT TURN 194 195  
 FT STRAND 196 200  
 FT STRAND 207 207  
 FT TURN 210 211  
 FT TURN 213 214  
 FT STRAND 216 219  
 FT TURN 220 221  
 FT STRAND 222 229  
 FT TURN 234 235  
 FT TURN 237 238  
 FT STRAND 241 245  
 FT HELIX 246 249  
 FT HELIX 250 258  
 FT TURN 259 259  
 SQ SEQUENCE 261 AA; 28998 MW; 4870748B174AF7C8 CRC64;

Query Match 47.3%; Score 595.5; DB 1; Length 261;  
 Best Local Similarity 44.5%; Pred. No. 7, 6e-48;  
 Matches 105; Conservative 46; Mismatches 78; Indels 7; Gaps 1;

QY 1 IIKGFECKPHSQWQALFEKTRLLCGATLAPRMLTAAHCKAPRYIVHLGQHNLOKE 60  
 DB 25 IVGGFCEKNSQWVAVAVYTOYLOGVLLDPNWLTAHCTDDNYKVLGKNLFDKE 84  
 QY 61 GCEQTRATESFPHGPNNSLPNK-----DHRNDIMLVKQASPVSTTAVRPLTSSR 113  
 DB 85 PSAQHFVSKAIPHPGFNMSIMRKHIFLEYDYSNDMLRLSKPADITDVKETLPTPE 144  
 QY 114 CVTAGTSCILSGWGTSSPOLRLPHLTRCANITIIHOCENAYPGNITDVMCASVQEG 173  
 DB 145 EPRDLSGTCLASGWSITPTPEQFTDLYCNVNLKLNEDOCARHAEKVTDAWLCAGEMDG 204  
 QY 174 GKSDCCGDSGGPVLVNCQSLQGLISWQODPCATRKPGVYTKVCKYVDWIOETMKNN 229  
 DB 205 KMDTKGDSGGPILCDGVIGITISWGHTPGCEPDMGVTTKLNKFTSWIKDMAXN 260

RESULT 14  
 ID TRY3 CHICK STANDARD; PRT; 248 AA.  
 AC Q90629;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 OS Gallus gallus (Chicken)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas; PubMed=7733885;  
 RA MEDLINE=95251611; "Isolation and characterization of the chicken trypsinogen gene family.";  
 RT Biochem. J. 307:471-479(1995).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Xaa, Lys-Xaa.  
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.

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 CC EMBL: U15157; AAA79914.1; -.  
 DR PIR: S55066; S55066.  
 DR HSR: F00763; IDPO.  
 DR MEROPS: S01.151; -.  
 DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYD\_SPC; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR Hydrolase: Serine protease; Digestion; Pancreas; Zymogen; Calcium-binding; Signal; Multigene family.

FT SIGNAL 1 16  
 FT PROPEP 17 25  
 FT CHAIN 26 248  
 FT ACT\_SITE 65 65  
 FT METAL 77 77  
 FT METAL 79 79  
 FT METAL 82 82  
 FT METAL 87 87  
 FT ACT\_SITE 109 109  
 FT ACT\_SITE 202 202  
 FT DISULFID 32 162  
 FT DISULFID 50 66  
 FT DISULFID 134 235  
 FT DISULFID 141 208  
 FT DISULFID 173 187  
 FT DISULFID 198 222  
 FT SITE 196 196  
 SQ SEQUENCE 248 AA; 26622 MW; E5E1B9076228588B CRC64;

Query Match 47.2%; Score 594; DB 1; Length 248;  
 Best Local Similarity 49.6%; Pred. No. 9, 9e-46;  
 Matches 112; Conservative 35; Mismatches 73; Indels 6; Gaps 3;

QY 1 IIKGFECKPHSQWQALFEKTRLLCGATLAPRMLTAAHCKAPRYIVHLGQHNLOKE 60  
 DB 26 IVGGTCEHSEVFPQVSL-NSGHHFCGSLNSQWVLSAAHCYSRQVRRGEVNIQVE 84  
 QY 61 GCEQTRATESFPHGPNNSLPNKDHRNDIMLVKQASPVSTTAVRPLTSSRCVTYGTG 120  
 DB 85 DSEVRRSSSVIRHPKYSITLN-----NDIMLVKQASPVSTTAVRPLTSSRCVTYGTG 140  
 QY 121 CLISGWSGTSSPOLRLPHLTRCANITIIHOCENAYPGNITDVMCASVQEGKDSGCG 180  
 DB 141 CLISGWSGTSSPOLRLPHLTRCANITIIHOCENAYPGNITDVMCASVQEGKDSGCG 200

QY 181 DSGPVLVNCNLSGQITISWGDDPCAIRKPGVYTKVCKYVDMIOETM 226  
DB 201 DSGPVLVNCNLSGQITISWGIG-CALXGYPGVYTKVCKYVDMIOETI 245

## RESULT 15

KLKR\_PRANA STANDARD; PRT; 263 AA.

AC P32824;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Glandular kallikrein, renal precursor (EC 3.4.21.35) (Tissue kallikrein).  
OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mastomys.  
OX NCBI\_Taxid=10112;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Salivary gland;  
RX MEDLINE=94226702; PubMed=7909667;  
RA Fahnestock M.;  
RT "Characterization of kallikrein cDNAs from the African rodent Mastomys.";  
RL DNA Cell Biol. 13:293-300(1994).  
CC -1- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release Lys-bradykinin.  
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of Met-Xaa or Leu-Xaa.  
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X17352; CA35232.1; -;  
DR PIR; I83227; S15686.  
DR HSP; P00757; 1SGF.  
DR MEROPS; S01.160; -;  
DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; trypsin\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydroxylase; Serine protease; Glycoprotein; Multigene family; Zymogen; Signal.  
FT SIGNAL 1 18  
FT PROPEP 19 24 PROBABLE.  
FT CHAIN 25 263 GLANDULAR KALLIKREIN, RENAL.  
FT ACT\_SITE 65 65 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 121 121 CHARGE RELAY SYSTEM.  
FT ACT\_SITE 215 215 CHARGE RELAY SYSTEM.  
FT DISULFID 31 175 BY SIMILARITY.  
FT DISULFID 50 66 BY SIMILARITY.  
FT DISULFID 153 221 BY SIMILARITY.  
FT DISULFID 186 200 BY SIMILARITY.  
FT DISULFID 211 236 BY SIMILARITY.  
FT CARBOHYD 102 102 N-LINKED (GLCNAC... ) (PROBABLE).  
SQ SEQUENCE 263 AA; 29130 MW; A8EB023B80037D5 CRC64;

Query Match 47.0%; Score 591.5; DB 1; Length 263;

Best Local Similarity 44.5%; Pred. No. 1.8e-47;  
Matches 106; Conservative 44; Mismatches 79; Indels 9; Gaps 2;  
QY 1 IIKGPECKPSQEPQOALFEKTRLLCGATIIAPRMLITAHCLKPRITVHLCQHNLQKE 60  
DB 25 IIGFNCENKSNQPMHVAVYRFAFYQCGVLLDANWVLTAAHCNDKXQVWLGNRRFEDE 84  
QY 61 GCEQTRATSEFPFGFNNSLPNKDH-----RNDIMLVKASPVSIWAVRPLTSS 112  
DB 85 PSAHQHLSKAIPIPGNMSLINDHCPHEEDYSDNMLVRLKPAETIDVYKPIDLPT 144  
QY 113 RCVTAGTISCLISNGSTS-SPQLRPLTLPCANITIEHCKENAPGNITDMVCAVQ 171  
DB 145 EEPYVGRCLASGWSITPTEEFYSHDLCCVYLELISNEVCAKAHTEKVTDTMLCGEM 204  
QY 172 EGGKDSQSGSGPVLVNCNLSGQITISWGDDPCAIRKPGVYTKVCKYVDMIOETMKN 229  
DB 205 DSGKDTGVDSGGPLICDGVLGQITISWGPFPALPNVPGIYTLIEYRSIKVWMANN 262

Search completed: June 22, 2004, 18:55:21  
Job time : 18 secs





EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO: 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-427

Query Match 100.0%; Score 1258; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.5e-125;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSOPMOMALFEKTRLLCGATLTAAPRWLTAACHLKRYIVHIGQNLQKEE 60  
DB 22 IIKGFECKPHSOPMOMALFEKTRLLCGATLTAAPRWLTAACHLKRYIVHIGQNLQKEE 81  
QY 61 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASVSIITWAVRPLTSSRCVTAAGTS 120  
DB 82 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASVSIITWAVRPLTSSRCVTAAGTS 141  
QY 121 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAVNGNITDTWVCAVVEGGKDSGCG 180  
DB 142 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAVNGNITDTWVCAVVEGGKDSGCG 201  
QY 181 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVKCYVDWIOETMKN 229  
DB 202 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVKCYVDWIOETMKN 250

RESULT 2  
US-09-025-059-1  
Sequence 1, Application US/09025059  
Patent No. 6075136

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGUT10  
CLONE: 2723646  
US-09-025-059-1

Query Match 100.0%; Score 1258; DB 3; Length 282;  
Best Local Similarity 100.0%; Pred. No. 1.8e-125;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSOPMOMALFEKTRLLCGATLTAAPRWLTAACHLKRYIVHIGQNLQKEE 60  
DB 54 IIKGFECKPHSOPMOMALFEKTRLLCGATLTAAPRWLTAACHLKRYIVHIGQNLQKEE 113  
QY 61 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASVSIITWAVRPLTSSRCVTAAGTS 120  
DB 114 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASVSIITWAVRPLTSSRCVTAAGTS 173  
QY 121 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAVNGNITDTWVCAVVEGGKDSGCG 180  
DB 174 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAVNGNITDTWVCAVVEGGKDSGCG 233  
QY 181 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVKCYVDWIOETMKN 229  
DB 234 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVKCYVDWIOETMKN 282

RESULT 3  
US-08-944-483-24  
Sequence 24, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COPIITS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.

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; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183. US. 01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-24

Query Match          97.5%; Score 1227; DB 3; Length 248;
Best Local Similarity 99.1%; Pred. No. 3e-122;
Matches 227; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 IIKGFEC-KPHSQWQALF-EKTRLLCGATLIAPRWLLTAACHCKPRYIVHLGQHNLOKE 60
DB 22 IIKGFEC-PIHSQWQALF-KTRLLCGATLIAPRWLLTAACHCKPRYIVHLGQHNLOKE 79
QY 61 GCEQTRRTATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 120
DB 80 GCEQTRRTATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 139
QY 121 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSQ 180
DB 140 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSQ 199
QY 181 DSGGPLVNCNQLGIIISWGDPCAITRKPGVYTKCKYVWIMQETMKN 229
DB 200 DSGGPLVNCNQLGIIISWGDPCAITRKPGVYTKCKYVWIMQETMKN 248

RESULT 4
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen

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; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORI-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14

Query Match          96.9%; Score 1219.5; DB 4; Length 289;
Best Local Similarity 97.0%; Pred. No. 2.3e-121;
Matches 223; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 IIKGFEC-KPHSQWQALF-EKTRLLCGATLIAPRWLLTAACHCKPRYIVHLGQHNLOKE 59
DB 52 IYGVNCLSKHSQPWQALF-EKTRLLCGATLIAPRWLLTAACHCKPRYIVHLGQHNLOKE 111
QY 60 ECEQTRRTATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 119
DB 112 ECEQTRRTATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 171
QY 120 SCLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSQ 179
DB 172 SCLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSQ 231
QY 180 DSGGPLVNCNQLGIIISWGDPCAITRKPGVYTKCKYVWIMQETMKN 229
DB 232 DSGGPLVNCNQLGIIISWGDPCAITRKPGVYTKCKYVWIMQETMKN 281

RESULT 5
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guesler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

```

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1020091  
US-09-025-059-3

Query Match 54.4%; Score 684; DB 3; Length 260;  
Best Local Similarity 53.1%; Pred. No. 1.5e-64;  
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAAPWLLTAHCKPRYIVHIGQNLQKEE 60  
DB 33 ILBERECIPHSQPMQALFQGERLICGVLVGDWRVLTAAHCKKQKSVRLGDSHSQSD 92  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKASPVSIWAAPLTLSSRCVTAGTS 120  
DB 93 QPEGEIIVAQSIQHPCYNNSNP-EDSHDMLIRLQNSANLGDKXRVOLANICPRVQOK 151  
QY 121 CLISGWSSTSPQRLPHTLRCAANTTIEHOKCENAPGNITPTMVCASVQEGKDCG 180  
DB 152 CLISGWSGTVTSPQENPNTLNCSEVKIYSONKCEBAPGKITEGMVCAG-SSNGADTCCG 210  
QY 181 DSGGPLVNCNLSGIIISMGDPCAITRKPGVYTKVCKYVDWIGETMKN 228  
DB 211 DSGGPLVCDGMLGIIISMGSDPCGKPKPGVYTKICRYTTWIKKTMDN 258

RESULT 6  
US-09-618-259-8  
Sequence 8, Application US/09618259  
Patent No. 6642013  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
FILE REFERENCE: D6020CIP2  
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
CURRENT APPLICATION NUMBER: US/09/618, 259  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: US 09/127,444  
PRIOR FILING DATE: 1998-08-21  
NUMBER OF SEQ ID NOS: 72  
SEQ ID NO 8  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURES:  
OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous  
OTHER INFORMATION: to TMDG-14; accession no. D30785  
US-09-618-259-8

Query Match 54.4%; Score 684; DB 4; Length 260;  
Best Local Similarity 53.1%; Pred. No. 1.5e-64;  
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAAPWLLTAHCKPRYIVHIGQNLQKEE 60  
DB 33 ILBERECIPHSQPMQALFQGERLICGVLVGDWRVLTAAHCKKQKSVRLGDSHSQSD 92  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKASPVSIWAAPLTLSSRCVTAGTS 120  
DB 93 QPEGEIIVAQSIQHPCYNNSNP-EDSHDMLIRLQNSANLGDKXRVOLANICPRVQOK 151  
QY 121 CLISGWSSTSPQRLPHTLRCAANTTIEHOKCENAPGNITPTMVCASVQEGKDCG 180  
DB 152 CLISGWSGTVTSPQENPNTLNCSEVKIYSONKCEBAPGKITEGMVCAG-SSNGADTCCG 210  
QY 181 DSGGPLVNCNLSGIIISMGDPCAITRKPGVYTKVCKYVDWIGETMKN 228

DB 211 DSGGPLVCDGMLGIIISMGSDPCGKPKPGVYTKICRYTTWIKKTMDN 258

RESULT 7  
US-09-070-526-2  
Sequence 2, Application US/09070526  
Patent No. 610059  
GENERAL INFORMATION:  
APPLICANT: SOUTHAN, CHRISTOPHER  
APPLICANT: CLINKENBEARD, HELEN  
APPLICANT: BURGESS, NICOLA  
TITLE OF INVENTION: No. 6100059el Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070, 526  
FILING DATE: 30-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9711952.3  
FILING DATE: 9-JUN-1997  
APPLICATION NUMBER: EP 97309646.4  
FILING DATE: 1-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-09-070-526-2

Query Match 54.1%; Score 681; DB 3; Length 260;  
Best Local Similarity 51.8%; Pred. No. 3e-64;  
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAAPWLLTAHCKPRYIVHIGQNLQKEE 60  
DB 33 VLGHECCPHSQPQWALFQGOQLLGGVLVGNWVLTAAHCKKPKYTVRLGDSLQNKD 92  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKASPVSIWAAPLTLSSRCVTAGTS 120  
DB 93 GPEQEIIVAVQSIHPHCYNNSS-DVEDHNDMLLQRLQASIGSKVKRISLADHTQGGX 151  
QY 121 CLISGWSSTSPQRLPHTLRCAANTTIEHOKCENAPGNITPTMVCASVQEGKDCG 180  
DB 152 CLISGWSGTVTSPREFFPTLNCASVKIIFPQKCEBAPGKITDGMVAGSSKGA-DTCG 210  
QY 181 DSGGPLVNCNLSGIIISMGDPCAITRKPGVYTKVCKYVDWIGETMKN 224  
DB 211 DSGGPLVCDGMLGIIISMGSDPCGKPKPGVYTKICRYTTWIKKTMDN 254

## RESULT 8

US-09-618-259-7  
Sequence 7, Application US/09618259  
Patent No. 6642013  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
FILE REFERENCE: D6020CIP2  
CURRENT APPLICATION NUMBER: US/09/618,259  
PRIORITY FILING DATE: 2000-07-18  
PRIORITY FILING DATE: 1998-08-21  
NUMBER OF SEQ ID NOS: 72  
SEQ ID NO 7  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of TADG-14 protein  
US-09-618-259-7

Query Match 54.1%; Score 681; DB 4; Length 260;  
Best Local Similarity 51.8%; Pred. No. 3e-64;  
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IIKGFECRPHSQPQWALFEKTRILCGATLIAPRMLITPAHCKPRYIVHIGQNLQKEE 60  
DB 33 VLGGEHCQPHSQPQWALFQGGQLCGVLVGNWVLTAAHCKKRYIVHIGDHSIQNKD 92  
QY 61 GCEQRTATSPFPHGNNSLPNKDRNDIMLVKMASPVSTIWAAYRPTLSRCVTAAGTS 120  
DB 93 GPEQELIPVQSIPIPCVNS-DVEDNHDMLQLRDQASLSGSKVPSLADHCTQPGOK 151  
QY 121 CLISGWSSTSPQLRPHLTRCANITIEHCKENAYPGNITDTMVCASVQEGGKDSQCG 180  
DB 152 CTVSGMGVTVSPRENFPDLTNCABEVKIFPQKKCEDAYGQITLDGVCAGSSKGA-DTCQG 210  
QY 181 DSGGPLVGNQSLQGIISWGQDPCATIRKPGVYTKVKCYVDWIOE 224  
DB 211 DSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDMIKK 254

## RESULT 9

US-09-008-271A-7  
Sequence 7, Application US/09008271A  
Patent No. 6203979  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Puryi  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271A  
FILING DATE: 16-Jan-1998  
PRIOR APPLICATION DATA:

## APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheila  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: COLNOT27  
CLONE: 1798496  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-008-271A-7

Query Match 53.5%; Score 673; DB 3; Length 260;  
Best Local Similarity 51.3%; Pred. No. 2.1e-63;  
Matches 115; Conservative 42; Mismatches 65; Indels 2; Gaps 2;

QY 1 IIKGFECRPHSQPQWALFEKTRILCGATLIAPRMLITPAHCKPRYIVHIGQNLQKEE 60  
DB 33 VLGGEHCQPHSQPQWALFQGGQLCGVLVGNWVLTAAHCKKRYIVHIGDHSIQNKD 92  
QY 61 GCEQRTATSPFPHGNNSLPNKDRNDIMLVKMASPVSTIWAAYRPTLSRCVTAAGTS 120  
DB 93 GPEQELIPVQSIPIPCVNS-DVEDNHDMLQLRDQASLSGSKVPSLADHCTQPGOK 151  
QY 121 CLISGWSSTSPQLRPHLTRCANITIEHCKENAYPGNITDTMVCASVQEGGKDSQCG 180  
DB 152 CTVSGMGVTVSPRENFPDLTNCABEVKIFPQKKCEDAYGQITLDGVCAGSSKGA-DTCQG 210  
QY 181 DSGGPLVGNQSLQGIISWGQDPCATIRKPGVYTKVKCYVDWIOE 224  
DB 211 DSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDMIKK 254

## RESULT 10

US-09-386-642-13  
Sequence 13, Application US/09386642  
Patent No. 6420157  
GENERAL INFORMATION:  
APPLICANT: Darlow, Andrew  
APPLICANT: Qi, Jensen  
APPLICANT: Andrade-Gordon, Patricia  
TITLE OF INVENTION: Zymogen Activation System  
FILE REFERENCE: ORT-1028  
CURRENT APPLICATION NUMBER: US/09/386,642  
PRIORITY FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-13

Query Match 53.4%; Score 671.5; DB 4; Length 288;  
Best Local Similarity 51.6%; Pred. No. 3.6e-63;  
Matches 116; Conservative 42; Mismatches 64; Indels 3; Gaps 3;

QY 1 IIKGFECRPHSQPQWALFEKTRILCGATLIAPRMLITPAHCKPRYIVHIGQNLQKEE 59  
DB 52 IIVGNCLEPHSQPQWALFQGGQLCGVLVGNWVLTAAHCKKRYIVHIGDHSIQNK 111

QY 60 ECGEQRRTATESFPHPGFENSLPNKDHNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 119  
Db 112 DGPEOEIPVVOISIPHPYNS -DVEDENHDMLOLRDQASLSKVKPISLADHCTQPOQ 170  
QY 120 SCISGSGTSPOLRLPHLRGANTITIEHOKCENAVPENITDTWVCA SVCEGSDSCQ 179  
Db 171 KCTVSGGTYSRENPNPDLNCAEVITFPKCEADAYRQGITDGNVCASSGA-DTQO 229  
QY 180 GDSGGLVNCNLSLOGITSWGDDPCATRKPGVYTKVYDWIOE 224  
Db 230 GDSGGLVNCNLSLOGITSWGSDPCGRSDKPGVYTNICRYDWIMK 274

RESULT 11  
US-09-205-258-1150  
Sequence 1150, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1150  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-1150

Query Match 51.7%; Score 651; DB 4; Length 228;  
Best Local Similarity 91.7%; Pred. No. 3,96-61;  
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 IIKGPECKPHSQPMQALFETRLLCGATLIAPRWMLTAHCLKPRITVHLGQNNLOKEE 60  
Db 4 IIKGPECKPHSQPMQALFETRLLCGATLIAPRWMLTAHCLKPRITVHLGQNNLOKEE 63  
QY 61 GCEQRTATESFPHPGFENSLPNKDHNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 120  
Db 64 GCEQRTATESFPHPGFENSLPNKDHNDIMLVKASPVSTWAVRPLTLSSRCVTAGT 123  
QY 121 CLISGSGTSP 132  
Db 124 CSFPAGARPDF 135

RESULT 12  
US-09-205-258-1149  
Sequence 1149, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06

Thu Jun 24 10:06:30 2004

us-09-856-320a-2\_copy\_54\_282.rat

Page 7

EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1149  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-205-258-1149  
Query Match  
Best Local Similarity 51.7%; Score 651; DB 4; Length 246;  
Best Local Similarity 91.7%; Pred. No. 4,3e-61;  
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
QY 1 IIKGFCEKPHSQPQALFEKTRILCGATLLAPRWLLTAHCKRKYVHJGQHNLOKEE 60  
DB 22 IIKGFCEKPHSQPQALFEKTRILCGATLLAPRWLLTAHCKRKYVHJGQHNLOKEE 81  
QY 61 GGEQRTATSESPHGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GGEQRTATSESPHGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSSTSP 132  
DB 142 CSFPAGAAPDP 153  
RESULT 13  
US-09-509-908-2  
; Sequence 2, Application US/09509908  
; Patent No. 6589770  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company, N/A N/A  
; TITLE OF INVENTION: A Protease  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: T. David Reed  
; STREET: 5299 Spring Grove Avenue  
; CITY: Cincinnati  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45217-1087  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/509,908  
; FILING DATE: 28-Feb-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, T. David  
; REGISTRATION NUMBER: 32,931  
; REFERENCE/DOCKET NUMBER: AA-264P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 513-627-7025  
; TELEFAX: 513-627-6333  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-509-908-2  
Query Match  
Best Local Similarity 51.2%; Score 644.5; DB 4; Length 293;  
Best Local Similarity 50.6%; Pred. No. 2.7e-60;  
Matches 117; Conservative 40; Mismatches 67; Indels 7; Gaps 4;  
QY 1 IIKGFCEKPHSQPQALFEKTRILCGATLLAPRWLLTAHCKRKYVHJGQHNLOK- 58  
DB 67 IINGSDCMHTQPMQDALLRPNQYCGAVLVHPQMLLTAHCKRKYVRLGHYSLSPV 126  
QY 59 EECGQRTATSESPHGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVTAG 118

Db 127 YESQGMFGVKSIFPHGYS---HFGHNDMLIKLNRRIRTKVPRINVSHPSPAG 182  
Qy 119 TSLISGWTSSPOLRPHLTRCANITIEHOKCENAYPGNITDTWVCASVQEGKSDC 178  
Db 183 TKCLVSGMGTSPQVAFPKVLQCLINISVLQKRCEDAYRQIDITWFCAG-DKAGRDSG 241  
Qy 179 QGDSGGLVNCOSIIGIISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 229  
Db 242 QGDSGGLVNCOSIIGIISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 292

## RESULT 14

US-08-824-874-1  
Sequence 1, Application US/08824874  
Patent No. 5862300  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
TITLE OF INVENTION: NOVEL KALLIKREIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/824,874  
FILING DATE: Filed Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0252 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: KERANOT02  
CLONE: 820694  
US-08-824-874-1

Query Match 47.5%; Score 597.5; DB 2; Length 268;  
Best Local Similarity 49.1%; Pred. No. 2.3e-55;  
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4;  
Qy 7 CKPHSQPMQALFEKTRLLGATLIAPRWLLTAHCLKPRYIVHIGQHNLOK-EEGGEOT 65  
Db 50 CTP-SRGAALLRPNDLYGCAVLYHPQMLTAHCKKRYRRLGHTISLPYESSGQM 108  
Qy 66 RTATESPFPHPFNNSLPKDRNDIMLVKASPVSIWAVRPLTSSRCVYTAGTSLISG 125  
Db 109 FGQVKSIFPHGYS---HFGHNDMLIKLNRRIRTKVPRINVSHPSPAGTKCLVSG 164  
Qy 126 WGSTSSPOLRPHLTRCANITIEHOKCENAYPGNITDTWVCASVQEGKSDGSGSGP 185  
Db 165 WGTKSPQVAFPKVLQCLINISVLQKRCEDAYRQIDITWFCAG-DKAGRDSGSGSGP 223

Qy 186 LVNCOSIIGIISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 229  
Db 224 VVNCOSIIGIISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 267

## RESULT 15

US-09-210-084-1  
Sequence 1, Application US/09210084  
Patent No. 6197511  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
TITLE OF INVENTION: NOVEL KALLIKREIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/210,084  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/824,874  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0252 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: KERANOT02  
CLONE: 820694  
US-09-210-084-1

Query Match 47.5%; Score 597.5; DB 3; Length 268;  
Best Local Similarity 49.1%; Pred. No. 2.3e-55;  
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4;  
Qy 7 CKPHSQPMQALFEKTRLLGATLIAPRWLLTAHCLKPRYIVHIGQHNLOK-EEGGEOT 65  
Db 50 CTP-SRGAALLRPNDLYGCAVLYHPQMLTAHCKKRYRRLGHTISLPYESSGQM 108  
Qy 66 RTATESPFPHPFNNSLPKDRNDIMLVKASPVSIWAVRPLTSSRCVYTAGTSLISG 125  
Db 109 FGQVKSIFPHGYS---HFGHNDMLIKLNRRIRTKVPRINVSHPSPAGTKCLVSG 164  
Qy 126 WGSTSSPOLRPHLTRCANITIEHOKCENAYPGNITDTWVCASVQEGKSDGSGSGP 185  
Db 165 WGTKSPQVAFPKVLQCLINISVLQKRCEDAYRQIDITWFCAG-DKAGRDSGSGSGP 223  
Qy 186 LVNCOSIIGIISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 229  
Db 224 VVNCOSIIGIISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 267



Thu Jun 24 10:06:30 2004

us-09-856-320a-2\_copy\_54\_282.rai

Page 9

Search completed: June 22, 2004, 18:57:27  
Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: June 22, 2004, 21:57:33 ; Search time 456 Seconds  
(without alignments)  
2133.415 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282  
Perfect score: 1258  
Sequence: 1 IIRGFBECKPHSGPWQALFE.....GVTTKYCKYVDWTQETMKNN 229

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 212409041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Command line parameters:

-MODEL=frame.p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US09856320/runat\_22062004\_172805\_1855/app.query.fasta\_1.391  
-DB=N-Geneseg\_29Jan04 -QMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=45  
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-USER=US09856320.cgn 1.1.885 @runat\_22062004\_172805\_1855 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEOUTERY -NES\_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WASN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
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#### Database :

N-Geneseg\_29Jan04:\*  
1: genesegn1980s:\*  
2: genesegn1998s:\*  
3: genesegn2000s:\*  
4: genesegn2001as:\*  
5: genesegn2001bs:\*  
6: genesegn2002as:\*  
7: genesegn2003as:\*  
8: genesegn2003bs:\*  
9: genesegn2003cs:\*  
10: genesegn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	1106	2	AA222638
2	1258	100.0	1158	2	AA222639
3	1258	100.0	1186	6	ABK92131
4	1258	100.0	1186	7	ABX76468
5	1258	100.0	1186	9	ADB80595
6	1258	100.0	1186	9	ADB75387
7	1258	100.0	1192	4	AAD14842
8	1258	100.0	1204	3	AAA37072

9	1258	100.0	1204	4	AA554320
10	1258	100.0	1204	4	AA521496
11	1258	100.0	1204	6	ABK33628
12	1258	100.0	1204	6	ABL68175
13	1258	100.0	1204	6	ABL95664
14	1258	100.0	1204	7	ACD24105
15	1258	100.0	1204	7	ACA66933
16	1258	100.0	1204	7	ACD68685
17	1258	100.0	1204	7	ACA67246
18	1258	100.0	1204	7	ACA03855
19	1258	100.0	1204	7	ABX89393
20	1258	100.0	1204	7	ACD42047
21	1258	100.0	1204	7	ACA68589
22	1258	100.0	1204	7	ACA04276
23	1258	100.0	1204	8	ADA46024
24	1258	100.0	1204	8	ADA76645
25	1258	100.0	1204	8	ABT44318
26	1258	100.0	1204	8	ADA19105
27	1258	100.0	1204	8	ADA61728
28	1258	100.0	1204	8	ADB19513
29	1258	100.0	1204	8	ADB28054
30	1258	100.0	1204	8	ADA86533
31	1258	100.0	1204	8	ADB16097
32	1258	100.0	1204	8	ADA47883
33	1258	100.0	1204	8	ACD68357
34	1258	100.0	1204	8	ADA67578
35	1258	100.0	1204	8	ADB30685
36	1258	100.0	1204	8	ADA85981
37	1258	100.0	1204	8	ADA97193
38	1258	100.0	1204	8	ADA79497
39	1258	100.0	1204	8	ADA87636
40	1258	100.0	1204	8	ADB16838
41	1258	100.0	1204	8	ADA91930
42	1258	100.0	1204	8	ADB14893
43	1258	100.0	1204	8	ADB18954
44	1258	100.0	1204	8	ADA94169
45	1258	100.0	1204	8	ADB20065

#### ALIGNMENTS

RESULT 1	AA222638	standard; cDNA; 1106 bp.
XX	AA222638	
AC	AA222638	
XX		
DT	08-DEC-1999	(first entry)
XX		
DE	CASB12 nucleotide sequence.	
XX		
KW	neurospn; cancer; assay; inhibitor; serine protease; immunogenic; ds.	
XX		
OS	Homo sapiens.	
XX		
FR	Key	Location/Qualifiers
FT	CDS	14..862
FT		/*tag= a
FT		/product= "CASB12"
XX		
PN	WO9949055-A1.	
XX		
PD	30-SEP-1999.	
XX		
PP	17-MAR-1999;	99WO-EP001894.
XX		
PR	20-MAR-1998;	98GB-00006095.
XX		
PA	(SMK ) SMITHKLINE BEECHAM BIOLOGICALS.	
XX		
PI	Bruck CEM, Cassart J, Coche T, Vinals-Bassols C,	
DR	WPI; 1999-580450/49.	



CC be used to diagnose the occurrence of tumor cells  
 XX  
 SQ Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	5.7e-104	1158
Percent Similarity:	1258.00	229
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
		Indels: 0
		Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AA222639 (1-1158)

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QY 1 llellelysglypneglucylslysprohisserglnproctpglnalaaleupheglu 20
DB 243 ATCATCAAGGGGTTGAGTGCAGCCCTCATCCAGCCCTGGCAGGAGCCCTTTCGAG 302
QY 21 lvsThrArgLeuLeuCySGlyAlaThLeuIleAlaProArgTrpLeuThrAla 40
DB 303 AAGACGGGGCTACTCTGTGGGGCGACCTCATCCGCCAGATGGCTCTCGACAGCAGCC 362
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysSGluGlu 60
DB 363 CACTGCTCTCAAGCCCGCTACATGATTCACTGGGGGAGCAACCTTCAGAAAGAGAG 422
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
DB 423 GGCTGTAGAGCAGACCCGAGACAGCAGTGAAGTCTTCCCCACCCCGCTTCAACAAACAGC 482
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 483 CTCCCAACAAAGCCACCCGAAATGACATCATGTGTGAAGATGGATGCCAGTCTCC 542
QY 101 lIethrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 543 ATCACTCGGGGTGTGGACACCCCTCATCCCTCCACAGCTGTGTCACTGCTGGCACACAGC 602
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 603 TGCTCTATTTCCGGCTGGGGGAGACACCTCCAGCCCGAGTTCAGCCCTCACACCTTG 662
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 160
DB 663 CGATGCCCAACATCACCACATCATTTGACACCCAGAAAGTGTAGAAGCCCTTACCCCGCAC 722
QY 161 lIethrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
DB 723 ATCACAAGACACCATGTGTGTGGCAGCGTCAGAAAGGGGGCAAGGACTCTCCCAAGGGT 782
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 783 GACTCCGGGGGCGCTCTGTGTGTGTACAGCTCTTAAAGCAATTCCTCTGGGGCGAG 842
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 220
DB 843 GATCCGTGTGATCAACCCGAAAGCTGTGTGTCAACGAAAGTGTGCAAAATGTGGAGC 962
QY 221 TrpIleGlnGlnThrMetLysAsnAsn 229
DB 903 TGGATCCAGAGAGATGAAGAACAAAT 929

```

## RESULT 3

ABK92131  
 ID ABK92131 standard; DNA; 1186 BP.

XX AC ABK92131;  
 XX 15-AUG-2002 (first entry)  
 DT Prostate cancer-associated DNA sequence #17.  
 DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;  
 KW

KW gene therapy; gene; ds.  
 XX Mammalia.  
 OS WO200230268-A2.  
 XX 18-APR-2002.  
 PD 12-OCT-2001; 2001WO-US032045.  
 XX 13-OCT-2000; 2000US-00687576.  
 PR 08-DEC-2000; 2000US-00733288.  
 PR 08-DEC-2000; 2000US-00733742.  
 PR 24-JAN-2001; 2001US-0263957P.  
 PR 16-MAR-2001; 2001US-0276791P.  
 PR 16-MAR-2001; 2001US-0276888P.  
 PR 06-APR-2001; 2001US-0281922P.  
 PR 24-APR-2001; 2001US-0286214P.  
 PR 30-APR-2001; 2001US-00847046.  
 PR 04-MAY-2001; 2001US-0288589P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;  
 PI MPI; 2002-471335/50.  
 XX P-PSDB; ABG61816.  
 DR  
 XX  
 XX  
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,  
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,  
 PT by determining if prostate cancer-associated genes are expressed in a  
 PT prostate tissue.  
 XX  
 XX  
 PS Claim 22; Page 313; 436pp; English.  
 XX  
 CC The present invention relates to methods of detecting a prostate cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC connecting a biological sample from the patient with prostate cancer-  
 CC associated polynucleotides (designated PC genes) that selectively  
 CC hybridise to a sequence that is at least 80% identical to them. The  
 CC prostate cancer-associated polynucleotide sequences are differentially  
 CC expressed in prostate tumour tissue or in prostate cancer and are derived  
 CC from the tissues of various organisms such as humans or other mammals  
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
 CC associated genes are useful for diagnosing or treating prostate cancer,  
 CC as well as for identifying modulators of prostate cancer or agents that  
 CC inhibit prostate cancer. The nucleic acid sequences are particularly  
 CC useful in gene therapy, as a vaccine or in antisense applications.  
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide  
 CC sequences  
 CC  
 SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	5.88e-104	1186
Percent Similarity:	1258.00	229
Best Local Similarity:	100.00%	Conservative: 0
Query Match:	100.00%	Mismatches: 0
		Indels: 0
		Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x ABK92131 (1-1186)

```

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QY 21 lvsThrArgLeuLeuCySGlyAlaThLeuIleAlaProArgTrpLeuThrAla 40
DB 245 AAGACGGGGCTACTCTGTGGGGCGACGCTCATCCGCCAGATGGCTCTCGACAGCAGCC 304
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysSGluGlu 60

```

Dd		305	CACCTGGCTCAAGCCCCCGTACTCATTAATTCACTTCGCGGAGCAGCAACCTCCAGAAAGAGAG	364
Oy		61	GlyCyseGluginThxArgThrAlaThrgIuseRpheProHisProGlyPheAsnSer	80
Dd		365	GGGTGTGAGAGACGCCGAGACGCACCTAGTGCTCTCCGCCACCCCGGCTTCACAACAGC	424
Oy		81	LeuProAsnLysAraSpHisArgAsnSerIleMetLeuValLysMetAlaSerProValSer	100
Dd		425	CTCCCCCAACAAAACACCGCATATCATCATGTGTGTGAAGAATGGCAATGCCAGTCTCC	484
Oy		101	IleThrTrpAlaValArxProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Dd		485	ATCACCTGGGGCTGTGTGACCCCTCAACCTCTCTCAAGCTGTGTGTACATGTGGACACAGC	544
Oy		121	CysLeuLileSerGlyYrTpolySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
Dd		545	TGCTCATTTTCCGGCGGGGAGACAGCTCCAGCCCCCAGTTACCGCTGTGCACACCTTG	604
Oy		141	ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaYrProGlyAsn	160
Dd		605	CGATGCCCACTCATCATCATCATTTAGACACCAAGAAAGTGTGAAGACGCTACCCGGCAC	664
Oy		161	IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly	180
Dd		665	ATCACAGACACCAATGGTGTGTGTGTGCACGCTGCAGGAAGGGGGCAGAGACTCTGTCCAGAGT	724
Oy		181	AspSerGlyGlyIyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	200
Dd		725	GACTCCGGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAAGCATTAATCTCTGGGGCAG	784
Oy		201	AspProCysAlaIleThrArgLysProGlyValYrThrLysValCysLysEtyrValAsp	220
Dd		785	GATCCGGTGTGCATCACCGAAAGCTGTGTGTCTACAGAAAGTGTGCAAAATATATGTGAC	844
Oy		221	TrpIleGlnIleThrMetLysAsnSer	229
Dd		845	TGGATCCAGAGACGATGAAGAACAAAT	871
RESULT 4				
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ID	ABX76468	standard; DNA; 1186 BP.		
AC	ABX76468;			
XX				
DT	02-APR-2003	(first entry)		
DE		Lung cancer-associated polynucleotide #332.		
XX				
KW		Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;		
KM		antiinflammatoary; antiaesthetic; non-small cell lung cancer; atelactasis;		
KW		small cell lung cancer; benign lesion; precancerous lesion; bronchitis;		
KM		chronic obstructive pulmonary disease; hypersensitivity pneumonitis;		
XX		interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.		
OS		Unidentified.		
XX				
FN	WO200286443-A2.			
XX				
PD	31-OCT-2002.			
XX				
PF	18-APR-2002; 2002MO-US012476.			
XX				
PR	18-APR-2001; 2001US-0284770P.			
PR	10-MAY-2001; 2001US-0280492P.			
PR	09-NOV-2001; 2001US-0319245P.			
PR	13-NOV-2001; 2001US-0350666P.			
PR	29-NOV-2001; 2001US-0334370P.			
PR	12-APR-2002; 2002US-0372246P.			
PA	(EOSB-) EOS BIOTECHNOLOGY INC.			
XX				
Pt	Aziz N. Murray R;			

XX	WPI; 2003-093161/08.
DR	P-PSDB; ABUS6739.
XX	Detecting a lung cancer-associated transcript in a cell from a patient
PT	for treating lung cancer, by contacting a biological sample from the
PT	patient with a polynucleotide that exhibits increased or decreased
XX	expression in lung cancer.
PS	Claim 22; Page 443; 453pp; English.
CC	The invention relates to a method for detecting a lung cancer-associated
CC	transcript in a cell from a patient, comprising contacting a biological
CC	sample from the patient with a polynucleotide that selectively hybridises
CC	to a sequence that is at least 80 % identical to a gene that exhibits
CC	increased or decreased expression in lung cancer samples. Lung cancer-
CC	associated polynucleotides and polypeptides are used for identifying a
CC	compound that modulates a lung cancer-associated polypeptide, for
CC	inhibiting proliferation of a lung cancer-associated cell to treat lung
CC	cancer in a patient and for treating a mammal having lung cancer by
CC	administering a modulatory compound identified. The methods are useful
CC	for treating lung cancer, such as small cell lung cancer, non-small cell
CC	lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC	emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC	hyperreactivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC	bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC	for diagnostic purposes and as targets for screening for therapeutic
CC	compounds that modulate lung cancer, such as antibodies. Sequences
CC	ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC	invention
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XX	
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Pred. No.:	5,886-104 Length: 1186
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Query Match:	100.00% Indels: 0
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Db	185 ATCATCAAGGAGTTTCAGTGCAGACCTCACCAGCCCTGGCAGGAGCCCTGTTCAG 244
QY	21 LysThrArgLeuLeuCySGLyAlaThrLeuilealaproagtlpleuLeuThrAlaIa 40
Db	245 AAGACGGCGCTACTCTGTGGGGCGACGCCCTCATCCGCCCAATGCTCTGCAGCGAGCC 304
QY	41 HisGlySerLeuArgProArgTrgTrlelaHlsleuglygnhsasleuLeuGlnLgLu 60
Db	305 CACGCGCTCAAGCCCCGCTCACATAAGTTCACTCTGGGGCAGCAAACCTCCAGAGAGAG 364
QY	61 GlCYsgsluGlInThrArghThAlathrguslerpheproHisPProgLyPheAsnAsnSer 80
Db	365 GGCTGTAGAGCAGACCCGGAACAGCACTGAGTCTTCCCACCCCGCTTCACAACAGC 424
QY	81 LeuProAsnLysAspHisArgAsnlnepillewelleuValysMetAlaserProValSer 100
Db	425 CTCGCCAACAAACACACCGCATATGACATCACTGGTGAAAGATGGCATGCCAGTCTCC 484
QY	101 lIethrTrpAlaValArgProLeuThrLeuSerSerArgCyVaIltnralgiYthrSer 120
Db	485 ATCACTCGGGCTGTGGACCCCTCAACCCCTCTCAAGCTGTGTGCACGTGGCACCAGC 544
QY	121 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuAlagleuProHisIthLeu 140
Db	545 TGCTCTCATTTTCGGCTGGGGCAGCACCTGCCACCCCGTAGTAACCTGTGCTCAACCTTG 604
QY	141 ArgGyvalAsnlnlethrllelleglnHlsGlnLysCySGLyAsnAlaTrPProgLYasn 160

50	Sequence 1166 BP; 272 A; 366 C; 302 G; 244 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	5,886-104
Score:	1258..00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
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Db	185 ATCATCAAGGGGTTTCAGTACGCAAGCCCTCACTCCCGGCTGGCGAGGAGCCCTGTTGAG 244
QY	21 LysHrArG1eu1eu1eu1ySg1yLa1rHr1eu1e1a1P1rO1q1T1P1e1u1Hr1a1a1a 40
Db	245 AAGAGCGGGTACTCTGCTGGGGCGAGCGCTCATCGCCCCCAATGGCTCTGACGACGACC 304
QY	41 HisCyS1eu1ySPrO1ArG1T1r1e1y1a1His1eu1yG1nH1sA1eu1yG1n1yS1u1n 60
Db	305 CACGCGCTCAAGCCCGCGTACATAGTTCACCTCGGGGCGACCAACCTCCAGAAAGAGAG 364
QY	61 GlyCySg1u1nH1rHr1rG1H1a1T1rG1uS1erP1eP1rO1H1sP1rO1y1P1he1a1nS1er 80
Db	365 GCGCTAGAGAGACCCGACGACGCCACTAGTCTCTCCCCACCCCGGCTTCAACACAGC 424
QY	81 LeuP1rO1a1n1yS1aP1H1s1ArG1a1nS1aP1l1e1u1e1u1a1y1S1e1r1a1a1SerP1rO1a1Ser 100
Db	425 CTCGCCAACAAGACCAACCGCAATAGACATCAACGCTGGTGAAGATGGCATGCCAGTCC 484
QY	101 Il1eHr1rP1a1y1a1ArG1P1rO1e1u1T1r1e1uS1erS1e1r1ArG1yS1a1l1Hr1a1G1y1ThrS1er 120
Db	485 ATCACTCGGGCTGTGCAACCCCTCAACCCCTCTCAAGCTGTGTACAGCTGGGACACAGC 544
QY	121 Cys1eu1leS1erG1y1T1pG1yS1erTh1rS1erS1erP1rO1G1n1e1u1a1rG1e1uP1rO1H1s1Th1r1e1u 140
Db	545 TGCCCTCATTTCCGGCTGGGCGACAGCTGCACACCCCGCTTACCGCTGCTCCACACCTTG 604
QY	141 ArgCySa1a1a1n1leHr1r1le1leG1nH1sG1n1yS1yS1a1e1u1a1y1P1rO1y1a1Sn 160

D6	605	CGATGGCCCAACATCCACATCATGATGAGCACAGAGTGTGAGAAAGCCTACCCGGAC	664
Qy	161	11eThAspPhrmetValCysAlaSerValGlnGlnGlyGlyValSerSerCysGlnGly	180
D6	665	ATACACACACCCATGGTGTGTGTGCACCGTGACGGAGAGGGGCGAAGGACTCTGCGACGGT	724
Qy	181	AspSerGlyValProLeuValCysAenGlnSerLeuGlnGlyLeuLeuSerTrpGlyGln	200
D6	725	GACTCCGGGGGCCCCCTGTGGCTGTACAGCTCTCTTCAAGCATTAATCTCTGGGGCGAG	784
Qy	201	AspProCysAlaIleThrArgLysProGlyValIleTrpLysValCysLysTrpValAsp	220
D6	785	GATCCGGGTGCGATCACCCGAAAGCCTGGTGTCTACAGAAAGTCTGCMAATATGTGAC	844
Qy	221	TrpIleGlnIleThrMetLysAsnAsn 229	
D6	845	TGGATCCAGAGACGATGAAACAAT 871	
RESULT 5			
ADB80595		ADB80595 standard; DNA; 1186 BP.	
XX	ADB80595:		
AC			
XX	04-DEC-2003	(first entry)	
DT			
XX			
DE		Ovarian cancer-associated transcript #81.	
XX			
KM		Cytosratic; gene therapy; vaccine; ovarian cancer; diagnosis;	
KM		post-operative chemotherapy; radiation therapy; tumour prognosis;	
KM		pre-cancerous lesion detection; ds; gene.	
XX			
OS		Homo sapiens.	
XX			
EH		Location/Qualifiers	
FT	Key	26, 874	
FT	CDS	/*tag= a	
XX			
FN		WO2002102235-A2.	
PD			
XX			
PF		18-JUN-2002; 2002MO-US019297.	
XX			
PR		18-JUN-2001; 2001US-0299234P.	
PR		27-AUG-2001; 2001US-0315287P.	
PR		05-SEP-2001; 2001US-0317544P.	
PR		13-NOV-2001; 2001US-0350666P.	
PR		12-APR-2002; 2002US-0372246P.	
XX			
PA		(EOSB-) EOS BIOTECHNOLOGY INC.	
XX			
PI		Mack DA, Gish KC;	
XX			
DR		WPI; 2003-16743/16.	
DR		P-PSDB; ADB80596.	
PT			
PT		Detecting an ovarian cancer-associated transcript in a cell from a	
PT		patient, comprises contacting a biological sample from the patient with a	
PT		polynucleotide that hybridizes to an ovarian cancer gene.	
XX			
PS		Claim 10; Page 328; 332pp; English.	
XX			
CC		The invention relates to a method of detecting an ovarian cancer-	
CC		associated transcript in a cell from a patient, by contacting a	
CC		biological sample from the patient with a polynucleotide that selectively	
CC		hybridizes to a sequence at least 80% identical to any of one of 80	
CC		nucleic acid sequences given in the specification. The method is useful	
CC		in diagnosing ovarian cancer and in identifying and using agents and/or	
CC		targets that inhibit ovarian cancer. The nucleic acid molecule,	
CC		polypeptide and the antibody may also be used in detecting ovarian	
CC		cancers, monitoring and early detection of relapse following treatment,	
CC		monitoring response to therapy, selecting patients for post-operative	

CC	chemotherapy or radiation therapy, in selecting mode of therapy,
CC	determining tumour prognosis, early detection of pre-cancerous lesions,
CC	and as vaccines. This sequence corresponds to one of the nucleic acids
CC	used for the detection method of the invention.
XX	
80	Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 U; 0 Other;
	Alignment Scores:
	Pred. No.: 5 88e-104 Length: 1186
	Score: 1258.00 Matches: 229
	Percent Similarity: 100.00% Conservative: 0
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	Query Match: 100.00% Indels: 0
	DB: 9 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ADB80595 (1-1186)	
QY	1 IleIleIleSgIyPheGluCysIysProHisSerGlnProTPGlnAlaAlaLeuPheGlu 20
Db	185 ATCTTCAGAGGGGATTTCAGAGTCAAGAGCTCTCACTCCAGCCCTGAGGAGCCCTTTGAG 244
QY	21 LysThrArgLeuLeuLeuYsgIyAlaThrLeuIleAlaProArgTPLeuLeuThrAlaAla 40
Db	245 AAGAGCGGGTACTCTGTGGGGGAGAGCTCATGCCCCGAGTGGCTCTCTACAGCGAGCC 304
QY	41 HisCysLeuIysProArgTyrTyrIleValHisLeuGlyGlnHisAsnLeuGlnIysGlu 60
Db	305 CACTGGCTCAAGCCCGGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAGAGAG 364
QY	61 GlyCysGlnGlnThrArgThrAlaThrGlnIysSerPheProHisProGlyIysPheAsnSer 80
Db	365 GGGTGTAGAGAGCCCGGAGCAGCACTGAGTCTTCTCCCAACCCCGGCTTCAACAAGC 422
QY	81 LeuProAsnIysAspHisArgAsnAspIleMetLeuValIysMetAlaSerProValSer 100
Db	425 CTCCCAACAGAAACACACCGCAGTACATCATGCTGGTGAAGATGGATGCCAGTCTCC 484
QY	101 IleThrTPAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThrSer 120
Db	485 ATCACTCGGGCTGTGGAGCCCTCAACCTCTCTCAAGCTGTGTCACTGTGGAGCAGC 544
QY	121 CysLeuIleSerGlyTyrPglIysSerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db	545 TGCTCATTTCCGGCTGGGGGAGCAGCTGCACCCCAAGTTCACGCTGCTCACTTG 604
QY	141 ArgCysAlaAsnIleThrIleIleGlnHisGlnIysCysGluAsnAlaTyrProGlyAsn 160
Db	605 CGATGCCCAACATCTCAACATCATTTGAGCAGCCAGAGTGTGAAGACGCTTACCCGAGC 664
QY	161 IleThrAspThrMetAlaCysAlaSerValGlnGlnIysGlyIysAspSerCysGlnGly 180
Db	665 ATCAACACACCCATGGTGTGTGTGCACAGCTGCAGAGAGGGGAGAGATCTCTGCCAGGCT 724
QY	181 AspSerGlyIysProLeuValCysAsnGlnSerLeuGlnIysIleIleSerTPGlyGln 200
Db	725 GACTCCGGGGGCGCTCTGGCTGTGAACCAAGTCTTCAAGGATATATCTCTGGGGCAG 784
QY	201 AspProCysAlaIleThrArgIysProGlyValTyrThrIysValCysIysTyrValAsp 220
Db	785 GATCCGGTGCATCAACCGAAGAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAGC 844
QY	221 TrpIleGlnIunThrMetIysAsnAsn 229
Db	845 TGCATCCAGAGAGCATGAAGAACAT 871
RESULT 6	
ADB75387	
XX	ADB75387 standard; cDNA; 1186 BP.
XX	ADB75387;
DT	04-DEC-2003 (first entry)
XX	

DB		Prostate cancer marker cDNA.
XX		
XX		Prostate; cancer; cytostatic; gene therapy; marker; ss.
KW		
OS	Homo sapiens.	
XX		
PN	WO2003009814-A2.	
PD		
XX	06-FEB-2003.	
PF		
XX	25-JUL-2002; 2002WO-US023913.	
PR		
XX	25-JUN-2001; 2001US-0307982P	
FR	22-AUG-2001; 2001US-0314356P	
XX	25-SEP-2001; 2001US-0325020P	
PR	12-DEC-2001; 2001US-0341746P	
XX	05-MAR-2002; 2002US-0362158P.	
PA	(MILL-) MILLENNIUM PHARM INC.	
P1	Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbarcheva B;	
P1	Hoernsh S, Kamatkar S, Monney AM, Glatt K, Zhao X, Anderson D,	
XX	WPI; 2003-248033/24.	
XX		
PT	New nucleic acid molecule, useful for diagnosing or treating prostate	
PT	cancer.	
XX		
BS	Disclosure; SEQ ID NO 211; 99pp; English.	
XX		
CC	The invention relates to newly discovered cancer markers associated with	
CC	the cancerous state of prostate cells. Also disclosed is a method of	
CC	assessing whether a patient is afflicted with prostate cancer. The method	
CC	of the invention involves assessing whether a patient is afflicted with	
CC	prostate cancer by comparing the level of expression of a marker in a	
CC	patient sample and the normal level of expression of the marker in a	
CC	control non-prostate cancer sample, where a significant increase in the	
CC	level of expression of the marker in the patient sample and the normal	
CC	level indicates that the patient is afflicted with prostate cancer.	
CC	Nucleic acids of the invention are useful for diagnosing or treating	
CC	prostate cancer, and may be useful in gene therapy. Sequences given in	
CC	ADB75177-ADB75611 represent marker cDNA and proteins. Note: The sequence	
CC	data for this patent did not form part of the printed specification, but	
CC	was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX		
SO	Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 U; 0 Other;	
XX		
	Alignment Scores:	
	Pred. No.: 5,88e-104 Length: 1186	
	Score: 1258.00 Matches: 229	
	Percent Similarity: 100.00% Conservative: 0	
	Best local Similarity: 100.00% Mismatches: 0	
	Query Match: 100.00% Indels: 0	
	DB: 9 Gaps: 0	
US-09-856-320A-2_COPY_54_282 (1-229) x ADB75387 (1-1186)		
OY	1 llelelrysglyphbegluCysLysProHisSerGlnProTyrpGlnAlaAleuPhegu 20	
Db	185 ATCATCAAGGGCTTCATGTGGGGGGAAGGCATCGGCCCAAGTGCTCTTACAGCACGC	244
OY	21 LysThrArgLeuleucYsgLyAlaThrLeulleAlaProArgTrpLeuLeuThAlaAla 40	
Db	245 AAAGCAGGGGCTACTCTGTGGGGGGAAGGCATCGGCCCAAGTGCTCTTACAGCACGC	304
OY	41 HisCysLeuLysProArGrTyrlileValHlsLeuGIyGlnHisAsnLeuGlnLysGLu 60	
Db	305 CACTGGCTCAAGCCCGCGCTACATAGTTCACTCGGGGAGACAACTCTCAAGAAGAGAG	364
OY	61 GlyCysGluGlnThrArgThralaThrGluSerPheProHisProGlyPheAsnAsrSer 80	
Db	365 GGCTGTGAGAGACCAGGACCGGACCACTGAGTCTTCCCCAACCCCGGCTTCACAAGAGC	424

Qy	81	IlePAsnLysAspHisArgHisnAsp11LeuLeuValLysMetAlaSerProValSer	100
Db	425	CTCCCAAAAGAACCCACCGCATATACATCATGCTGGTGAAGATGGCATGCCAGTCTCC	484
Qy	101	IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Db	485	ATCACCCTGGCGCTGTGGACCCCTCACCCCTCTCTCCACCGCTGTCTCAGCTGGACACAGC	544
Qy	121	CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
Db	545	TGCTCTATTTCGGCTGGGGCGACACGCTCCAGCCCCAGTTACGCCCTGGCTCACACCTTG	604
Qy	141	ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaIlyProGlyAsn	160
Db	605	CGATGGCGCAATCATCACCATCTATTAGCACACAGAAAGTGTGAAAGCGCTCACCCCGGCAC	664
Qy	161	IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly	180
Db	665	ATACAGACACCATGGTGTGTGTCCAGCGCTGCAGAGAGGGGCAAGAGCTCTGCCAGGCT	724
Qy	181	AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	200
Db	725	GACTCCGGGGGCGCTCTGGTCTGTATACAGACTCTCTTCAGGCGCATATCTCTGGGGCAG	784
Qy	201	AspProCysAlaIleThrArgLysProGlyValIlyThrLysValCysLysIlyTrpAlaAsp	220
Db	785	GATCCGGTGTGCATCACCCGAAAGCGCTGTGTCTTACAGAAAGTCTCCAAATATGTGAC	844
Qy	221	TrpIleGlnGluThrMetLysAsnAsn	229
Db	845	TGGATCCAGAGACGATGAAAGACAT	871
RESULT 7			
AD14842			
ID	AD14842 standard; DNA; 1192 bp.		
XX			
AC	AAD14842;		
XX			
DT	01-NOV-2001 (first entry)		
XX			
DE	Human PS133 gene contig.		
XX			
KW	Human; PS133; prostate disease; cancer; immunogen; gene therapy; EST;		
KW	expressed sequence tag; cytosstatic; ds.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	107..859		
FT	/*tag= a		
FT	/product= "Human PS133 protein"		
FT	/transl_except= (pos:188..196, aa:Cys-Pro)		
FT	/transl_except= (pos:224..232, aa:Phe-Lys)		
XX			
PN	US6232456-B1.		
XX			
PD	15-MAY-2001.		
XX			
PF	06-OCT-1997; 97US-00944483.		
XX			
PR	06-OCT-1997; 97US-00944483.		
XX			
PA	(ABBO ) ABBOTT LAB.		
XX			
XX	Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;		
PI	Russell JC, Stewart KD, Stroupe SD;		
XX			
DR	WP1: 2001-366357/38.		
XX			
DR	P-PSDB; AAB08017.		
XX			
FT	New PS133 polynucleotides, useful for detecting, diagnosing, staging,		
FT	monitoring, prognostic, preventing, treating or determining the		





PR 24-SEP-1998; 98US-0101741P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 24-SEP-1998; 98US-0101915P.  
 PR 24-SEP-1998; 98US-0101916P.  
 PR 29-SEP-1998; 98US-0102207P.  
 PR 29-SEP-1998; 98US-0102240P.  
 PR 29-SEP-1998; 98US-0102307P.  
 PR 29-SEP-1998; 98US-0102331P.  
 PR 29-SEP-1998; 98US-0102331P.  
 PR 30-SEP-1998; 98US-0102484P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 30-SEP-1998; 98US-0102571P.  
 PR 01-OCT-1998; 98US-0102684P.  
 PR 01-OCT-1998; 98US-0102687P.  
 PR 02-OCT-1998; 98US-0102965P.  
 PR 06-OCT-1998; 98US-0103258P.  
 PR 07-OCT-1998; 98US-0103314P.  
 PR 07-OCT-1998; 98US-0103315P.  
 PR 07-OCT-1998; 98US-0103385P.  
 PR 07-OCT-1998; 98US-0103385P.  
 PR 07-OCT-1998; 98US-0103386P.  
 PR 07-OCT-1998; 98US-0103401P.  
 PR 08-OCT-1998; 98US-0103633P.  
 PR 08-OCT-1998; 98US-0103678P.  
 PR 08-OCT-1998; 98US-0103679P.  
 PR 08-OCT-1998; 98US-0103711P.  
 PR 14-OCT-1998; 98US-0104257P.  
 PR 20-OCT-1998; 98US-0104987P.  
 PR 20-OCT-1998; 98US-0105000P.  
 PR 20-OCT-1998; 98US-0105002P.  
 PR 21-OCT-1998; 98US-0105104P.  
 PR 22-OCT-1998; 98US-0105169P.  
 PR 22-OCT-1998; 98US-0105263P.  
 PR 26-OCT-1998; 98US-0105633P.  
 PR 26-OCT-1998; 98US-0105634P.  
 PR 27-OCT-1998; 98US-0105807P.  
 PR 27-OCT-1998; 98US-0105881P.  
 PR 27-OCT-1998; 98US-0105882P.  
 PR 27-OCT-1998; 98US-0106062P.  
 PR 28-OCT-1998; 98US-0106023P.  
 PR 28-OCT-1998; 98US-0106023P.  
 PR 28-OCT-1998; 98US-0106030P.  
 PR 28-OCT-1998; 98US-0106030P.  
 PR 28-OCT-1998; 98US-0106032P.  
 PR 28-OCT-1998; 98US-0106033P.  
 PR 28-OCT-1998; 98US-0106178P.  
 PR 29-OCT-1998; 98US-0106248P.  
 PR 29-OCT-1998; 98US-0106384P.  
 PR 29-OCT-1998; 98US-0108500P.  
 PR 30-OCT-1998; 98US-0106464P.  
 PR 03-NOV-1998; 98US-0106856P.  
 PR 03-NOV-1998; 98US-0106902P.  
 PR 03-NOV-1998; 98US-0106905P.  
 PR 03-NOV-1998; 98US-0106919P.  
 PR 03-NOV-1998; 98US-0106932P.  
 PR 03-NOV-1998; 98US-0106934P.  
 PR 10-NOV-1998; 98US-0107783P.  
 PR 17-NOV-1998; 98US-0108775P.  
 PR 17-NOV-1998; 98US-0108779P.  
 PR 17-NOV-1998; 98US-0108787P.  
 PR 17-NOV-1998; 98US-0108788P.  
 PR 17-NOV-1998; 98US-0108801P.  
 PR 17-NOV-1998; 98US-0108802P.  
 PR 17-NOV-1998; 98US-0108806P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.

PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 XX WPI; 2000-237871/20.  
 DR P-PSDB; AAY99390.  
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX  
 PS Claim 2; Fig 101; 773pp; English.  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention  
 XX  
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5,99e-104 Length: 1204.  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 3  
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 QY 1 Iletlelysglyphgheglucyalyserphrohisserglnpctpglnaiaaleupheglu 20  
 DB 169 ATCATCAAGGGGTTGGAGTGAAGCTCACTCCAGCCCTGGAGGCGCTGTTCCAG 228  
 QY 21 LysThrArgLeuLeuCyseGlyAlaThrLeuLeuAlaProArgTrpLeuThrAla 40  
 DB 229 AAGACGGCGCTACTGTGGGGCGACGCTCACTCCAGCAATGAGCTCTCAACAGAGCC 288  
 QY 41 HisCysLeuysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnGlyGlu 60  
 DB 289 CACTGCCCTCAAGCCCCCGCTCACTAGTTCACCTGGGGGAGCAACCTTCAGAGGAGG 348  
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisPheAsnAsnSer 80  
 DB 349 GGCTGTGAGCAGACCCGAGCAGCCCTAGTCCTTCCCCCAGCCCGGCTTCAACAGAGC 408  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 DB 409 CTCCCAACAAAGACCAACCGCATGATGCTGCTGGAAGATGATGATCCAGCTCC 468  
 QY 101 IletHrTPAlaValArgProLeuThrLeuSerArgCysValThrAlaGlyThSer 120  
 DB 469 ATCACTGGGCTGTGAGCAGCCCTCACTCTCACTGCTGTGCTGCTGCTGCTGCTGCTG 528  
 QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 DB 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTCAAGCCCAAGCTTACGCTCTCTCAACCTTG 588  
 QY 141 ArgCysAlaAsnIleThrIleIleLeuHisGlnLysCysGlyAsnAlaTyrProGlyVal 160  
 DB 589 CGATGGCGCCACATACATCATTAAGACCAAGAGTGTGAAGAGCTTACCCCGGCAAC 648  
 QY 161 IletHrAspThrMetValCysAlaSerValGlnGlnGlyGlyAspSerCysGlnGly 180  
 DB 649 ATCAAGACACCATGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708

QY 161 AsperglyglyProleuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGGCGCTCTGGTCTGTACCAAGCTCTTCAAGGCAATATCTCTCGGGGCGAG 768  
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220  
 Db 769 GATCCGGTGTGGATCACCCGAAAGCCTGGTGTACACGAAAGTCTGCAATATATGTGGAC 828  
 QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
 Db 829 TGGATCCAGAGACGATGAAGAACAAAT 855  
 RESULT 9  
 AAF54320  
 ID AAF54320 standard; DNA; 1204 BP.  
 AC AAF54320;  
 XX 02-APR-2001 (first entry)  
 DT DNA encoding protein of the invention #51.  
 DE DNA encoding protein of the invention #51.  
 XX Secreted; transmembrane; gene therapy; ss.  
 KM  
 XX Unidentified.  
 OS  
 XX WC0200078961-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 18-FEB-2000; 2000WC-US004342.  
 PF  
 XX 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028513.  
 PR 02-DEC-1999; 99WO-US030095.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WC-US000219.  
 PR 06-JAN-2000; 2000WC-US000376.  
 PA  
 XX (GENTH ) GENENTECH INC.  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams FM, Wood WI;  
 XX WPI; 2001-071395/08.  
 DR  
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX  
 PS Claim 2; Fig 101; 787pp; English.  
 XX  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 CC  
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 5.99e-104 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AAF54320 (1-1204)  
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 Db 169 ATCATCAAGGGGTTGATGACAGCTCACTCCAGCCCTGGACAGCGACCTGTTCCAG 228  
 QY 21 LysThrArgLeuLeuCysGlyValAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40  
 Db 229 AAGACGGCGCTACTCTGTGGGGCGACGCTCACTCCGCGACATGGCTCTCTGACACAC 288  
 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60  
 Db 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGACACACCTCCAGAGGAGAG 348  
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisSerProGlyPheAsnAsnSer 80  
 Db 349 GGCTGTGACGACACCGGACAGCCACTGAGTCTTCCCGACCCCGGCTTCAACACAGC 408  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 409 CTCCCAACAAAGACACCGCATATCATGCTGTGGATGATGCAATCGCCAGATCTCC 468  
 QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 469 ATCACTGGGCTGTGTGACCCCTCACTCTCTCTCACTGTGTGTGTGTGTGTGTGTGTGT 528  
 QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 529 TGCCTCATTTCCGGCTGGGGCGACAGCTGCAGCCCGCCAGTTAAGCTCTCTCACACCTTG 588  
 QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160  
 Db 589 CGATCGGCCACATATCACTATGTAGACCAAGAGTGTAGAACGCTTACCCCGGACAC 648  
 QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
 Db 649 ATCAACAGACACCATGT 708  
 QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGGCGCTCTGGTCTGTACCAAGCTCTTCAAGGCAATATCTCTCGGGGCGAG 768  
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220  
 Db 769 GATCCGGTGTGGATCACCCGAAAGCCTGGTGTACACGAAAGTCTGCAATATATGTGGAC 828  
 QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
 Db 829 TGGATCCAGAGACGATGAAGAACAAAT 855  
 RESULT 10  
 AAS21496  
 ID AAS21496 standard; cDNA; 1204 BP.  
 XX  
 AC AAS21496;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DT Human cDNA sequence encoding for PRO1279 polypeptide.  
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 XX prostate; cervical; tumor necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIA; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WC0200140466-A2.  
 XX

07-JUN-2001.  
 01-DEC-2000; 2000WO-US032678.  
 01-DEC-1999; 99WO-US028301.  
 01-DEC-1999; 99WO-US028634.  
 02-DEC-1999; 99WO-US028551.  
 02-DEC-1999; 99WO-US028564.  
 02-DEC-1999; 99WO-US028565.  
 09-DEC-1999; 99US-0170282P.  
 16-DEC-1999; 99WO-US030095.  
 20-DEC-1999; 99WO-US030911.  
 20-DEC-1999; 99WO-US031243.  
 30-DEC-1999; 99WO-US031274.  
 05-JAN-2000; 2000WO-US000219.  
 06-JAN-2000; 2000WO-US000277.  
 06-JAN-2000; 2000WO-US000376.  
 11-FEB-2000; 2000WO-US003565.  
 18-FEB-2000; 2000WO-US004341.  
 18-FEB-2000; 2000WO-US004342.  
 22-FEB-2000; 2000WO-US004314.  
 24-FEB-2000; 2000WO-US004504.  
 24-FEB-2000; 2000WO-US005504.  
 01-MAR-2000; 2000WO-US005501.  
 02-MAR-2000; 2000WO-US005541.  
 03-MAR-2000; 2000US-0187202P.  
 10-MAR-2000; 2000WO-US006319.  
 15-MAR-2000; 2000WO-US006884.  
 20-MAR-2000; 2000WO-US007377.  
 21-MAR-2000; 2000WO-US007532.  
 30-MAR-2000; 2000WO-US008439.  
 17-MAY-2000; 2000WO-US013705.  
 22-MAY-2000; 2000WO-US014042.  
 30-MAY-2000; 2000WO-US014941.  
 02-JUN-2000; 2000WO-US015264.  
 05-JUN-2000; 2000US-0209832P.  
 28-JUL-2000; 2000WO-US020710.  
 11-AUG-2000; 2000WO-US020231.  
 23-AUG-2000; 2000WO-US023522.  
 24-AUG-2000; 2000WO-US023328.  
 08-NOV-2000; 2000WO-US030952.  
 10-NOV-2000; 2000WO-US030873.  
 (GENTH ) GENENTECH INC.  
 Baker KP, Barresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Guirney AL, Sherwood S, Smith V, Stewart TX, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2001-408281/43.  
 P-PSDB; AAU12424.  
 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.  
 Claim 3; Fig 505; 813pp; English.  
 AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumors by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes

(PEMCS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy

Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	Length:	Matches:
5,99e-104	1204	229
Score:	1258.00	Conservative: 0
Percent Similarity:	100.00%	Mismatches: 0
Best Local Similarity:	100.00%	Indels: 0
Query Match:	100.00%	Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x AAS21496 (1-1204)

QY	1	IleIleIleYsgIYphneIuCYsLYsPProHISerGInProTTPGInAlaIaleuPheGlu	20
DB	169	ATCATCAAGGGGATTGAGTGCAGACCTCCAGCCCTGGCAGGACGCTCTTCCAG	228
QY	21	LysThrArgLeuLeuCYsGlyAlaThrIleuIleIleProArgTyrLeuThrAlaAla	40
DB	229	AAGACGCGCTACTCTGTGGGCGAGCGTCACTCCCGCAATGCTCTTCCAGCAGCC	288
QY	41	HisCYsLeuYsPProArgTyrIleValHisLeuIleGlnHisAsnLeuGlnIleGlu	60
DB	289	CACCTCCCTCAAGCCCGGCTCATATGTTACCTGGGCGACCACTCCAGGAAGAGAG	348
QY	61	GlyCYsGluGlnThrArgThrAlaThrGluSerPheProHisPProGlyPheAsnSer	80
DB	349	GGCTGTGAGCAGACCCGAGCAGCCAGCTAGCTTCCCGCCCGGCTTAAACAACAC	408
QY	81	LeuProAsnYsAspHisArgAsnAspIleMetLeuValYsMetAlaSerProValSer	100
DB	409	CTCCCAACCAAGACCAACCGATGACATCTGCTGGAGAGATGGCATGGCATCTCC	468
QY	101	IleThrTPAlaValArgProLeuThrIleuSerSerArgCYsValThrAlaGlyThrSer	120
DB	469	ATCACCTGGGCTGTGCGACCCCTCACTCTCCACCTGTGTACGTGGCAGCAGC	528
QY	121	CysLeuIleSerGlyThrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
DB	529	TGCTTCATTTCCGCTGGGCGAGCGTCCAGCCCGGCTTACCGCTCCACACCTTG	588
QY	141	ArgCYsAlaAsnIleThrIleIleGlnHisGlnYsCYsGluAsnAlaTyrProGlyAsn	160
DB	589	CGATCGGCAACATCACCATTGAGCAGCAGAAAGTGTGAGAACGCTTACCCGCGCAC	648
QY	161	IleThrAspThrMetValCYsAlaSerValGlnGlnIleGlyYsAspSerCYsGlnGly	180
DB	649	ATCACAGACACCATGCTGTGTCCAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGG	708
QY	181	AspSerGlyGlyProLeuValCYsAsnGlnSerLeuGlnIleIleSerTyrGlyGln	200
DB	709	GATCCGGGGGCGCCCTGCTGTGTAACAGCTCTTCAAGCATATATCTCGGGGCGAG	768
QY	201	AspProCYsAlaIleThrArgLYsPProGlyValTyrThrIleValCYsLYsTyrValAsp	220
DB	769	GATCCGTGGCATCACCAGGAGGCTGTGTCTTACAGAAAGTGTGCAAAATATGTGAC	828
QY	221	TyrIleGlnGlnThrMetLYsAsnAsn	229
DB	829	TGATTCAGAGACATGATGAGACAT	855

RESULT 11  
 ABEK33628 standard; cDNA; 1204 BP.  
 ID ABEK33628  
 AC ABEK33628;

XX 08-MAY-2002 (first entry)  
DT CDNA encoding human PRO protein, Seq ID No 185.  
XX  
DE  
XX  
KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KM breast cancer; prostate tumour; rectal tumour; liver tumour;  
KM pericyte cell proliferation; chondrocyte cell proliferation;  
KM tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PP 29-JUN-2001; 2001WO-US021066.  
XX  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220585P.  
PR 25-JUL-2000; 2000US-0220605P.  
PR 25-JUL-2000; 2000US-0220607P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220638P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 25-JUL-2000; 2000US-0220666P.  
PR 26-JUL-2000; 2000US-0220893P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-AUG-2000; 2000US-0222425P.  
PR 23-AUG-2000; 2000US-0227133P.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 28-NOV-2000; 2000US-0253646P.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854288.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gutney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-172001/22.  
DR P-PSDB; AAU83684.  
XX  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumors such  
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor  
PT or liver tumor.  
XX  
PS Claim 2; Fig 185; 359bp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumors, especially lung  
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
CC liver tumor. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes.

CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO  
CC protein coding sequences of the invention  
XX  
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 5,99e-104 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 6  
US-09-856-320a-2\_COPY\_54\_282 (1-229) x ABK33628 (1-1204)  
QY 1 IleIleIleGlyPheGluCysIleProHisSerGlnProTyrGlnAlaIleLeuPheGlu 20  
DB 169 ATCATCAAGGGGTTCAGTGAAGCCTCACTCCAGCCTGGCAGGCACTGTCGAG 228  
QY 21 LysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTyrLeuThrAlaIle 40  
DB 229 AAGACCGGCTACTCTGTGGGGGAGCGCTCATGCCCCAGATGGCTCTGACAGAGCC 288  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnIleGlu 60  
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGACACACTCCAGAGAGAGG 348  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80  
DB 349 GGCTGTGACAGAGCCCGGACAGCCACTGATGCTTCCCCACCCGGCTTCAACAGAC 408  
QY 81 LeuProAsnLysAspHisArgAsnSerIleMetLeuValIleMetAlaSerProValSer 100  
DB 409 CTCGCCAAGAACACCCGCAATGATCATGCTGTGAAGATGGCATCGCACTGCC 468  
QY 101 IleThrTyrAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTGGGCTGTGGACCCCTCACTCTCTCTCACTGTGCTGCTGCTGCTGCTGCTG 528  
QY 121 CysLeuIleSerGlyTyrProLysSerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCTCATTTCCGGCTGGGGGAGCAGCTCACTCCCACTTACGCTGCTCACTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
DB 589 CGATCGCCCAATCATCATCATTTGAGCACAGAAAGTGTGAGAAAGCCCTACCCGGCAAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerGlyGlnGly 180  
DB 649 ATCAACAGACACCATGTGTGTCCAGCCGTGACGGAAGGGGCAAGAGACTCCGACGGGT 708  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln 200  
DB 709 GATTCGGGGGCGCTCTGT 768  
QY 201 AspProCysAlaIleThrArgLysProGlyValIleTyrThrLysValCysLysTyrValAsp 220  
DB 769 GATCCGCTGTGCAATCACTCCGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828  
QY 221 TrrIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACATGAAAGACANT 855  
RESULT 12  
ABL88175  
ID ABL88175 standard; cDNA; 1204 BP.  
XX  
AC ABL88175;  
XX  
XX 16-MAY-2002 (first entry)  
DT  
XX  
DE Human PRO1279 cDNA sequence SEQ ID NO:207.  
XX

KM	Human, angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KM	vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KM	gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KM	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KM	age-related macular degeneration; arterial resensitization; angina;
KM	rheumatoid arthritis; myocardial infarction; thrombopilepsis;
KM	lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;
KM	wound healing; chromosome mapping; gene mapping; gene, ss.
OS	Homo sapiens.
XX	
PN	WO200200690-A2.
XX	
PD	03-JAN-2002.
XX	
PF	20-JUN-2001; 2001WO-US019692.
XX	
XX	23-JUN-2000; 2000US-0213637P.
PR	20-JUL-2000; 2000US-0219556P.
PR	25-JUL-2000; 2000US-0220624P.
PR	25-JUL-2000; 2000US-0220664P.
PR	28-JUL-2000; 2000WO-US020710.
PR	02-AUG-2000; 2000US-0222695P.
PR	17-AUG-2000; 2000US-00643657.
PR	23-AUG-2000; 2000WO-US023522.
PR	24-AUG-2000; 2000WO-US023328.
PR	07-SEP-2000; 2000US-0230978P.
PR	18-SEP-2000; 2000US-00654610.
PR	18-SEP-2000; 2000US-00655350.
PR	24-OCT-2000; 2000US-0245222P.
PR	08-NOV-2000; 2000US-00709238.
PR	08-NOV-2000; 2000WO-US030952.
PR	10-NOV-2000; 2000WO-US030873.
PR	01-DEC-2000; 2000WO-US032678.
PR	20-DEC-2000; 2000US-00747259.
PR	20-DEC-2000; 2000WO-US034956.
PR	22-JAN-2001; 2001US-00767609.
PR	28-FEB-2001; 2001US-00796498.
PR	28-FEB-2001; 2001WO-US006520.
PR	01-MAR-2001; 2001WO-US006666.
PR	09-MAR-2001; 2001US-00802706.
PR	14-MAR-2001; 2001US-00806889.
PR	22-MAR-2001; 2001US-00816744.
PR	05-APR-2001; 2001US-00828366.
PR	10-MAY-2001; 2001US-00854208.
PR	10-MAY-2001; 2001US-00854280.
PR	25-MAY-2001; 2001US-00866028.
PR	25-MAY-2001; 2001US-00866034.
PR	25-MAY-2001; 2001WO-US017092.
PR	30-MAY-2001; 2001US-00870574.
PR	30-MAY-2001; 2001WO-US017443.
PR	01-JUN-2001; 2001WO-US017800.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Baker KP, Ferrara N, Gerber H, Gertlsen ME, Goddard A, Paoni NF;
PI	Godowski PU, Gurney AL, Hillan KJ, Masters SA, Pan J, Ye W;
PI	Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;
XX	
XX	WPI; 2002-090516/12.
DR	P-PSDB; ABB84920.
XX	
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal.
XX	
PS	Claim 2; Fig 207; 565pp; English.
XX	
CC	AB188072 to AB188258 encode the PRO proteins given in ABB84817 to
CC	AB1885003. The PRO proteins and polynucleotides have cardiac, cytosolic,
CC	antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agonists and antagonists are useful for treating or diagnosing

CC	cardiovascular, endothelial oxangemic disorder in a mammal, e.g.
CC	cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC	healing. The p80 polynucleotides have applications in molecular biology,
CC	including use as hybridisation probes, and in chromosome and gene
CC	mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	5.99e-104
Score:	1258.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
DB:	Gaps: 0
US-09-8556-320A-2_COPY_54_282 (1-229) x ABL88175 (1-1204)	
QY	1
Db	169
QY	21
Db	229
QY	41
Db	289
QY	61
Db	349
QY	81
Db	409
QY	101
Db	469
QY	121
Db	529
QY	141
Db	589
QY	161
Db	649
QY	181
Db	709
QY	201
Db	769
QY	221
Db	829



QY 201 AspProCysAlaIleThraArgLysProGlyValIleTyrThrLysValCysLysTyrValAsp 220  
DB 769 GATCGCTGCGATACCCGAAAGCCTGATGCTTACGAAAGTCTGCAAAATATGTGAC 828  
QY 221 TTTTLeGlnGluThrMetLysAsn 229  
DB 829 TGGATCCAGAGACGATGAAGAACAT 855

RESULT 14  
ACD24105  
ID ACD24105 standard; cDNA; 1204 BP.  
XX  
AC ACD24105;  
XX  
DT 26-AUG-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO1279 cDNA.  
XX  
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;  
XX antiarteriosclerotic; cardiact; anti-infertility; anti-HIV; cytostatic;  
XX antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
XX TNF-alpha release; cell proliferation; cell differentiation;  
XX gene expression modulator; proteoglycan release; atherosclerosis;  
XX tumour; inflammatory disease; organ failure; premature aging; AIDS;  
XX cardiac injury; infertility; birth defect; prematurity; cancer; diabetic complication;  
XX acquired immunodeficiency syndrome; cancer; diagnostic; biosensor;  
XX chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
XX bioreactor; tissue typing; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2003032156-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 06-MAY-2002; 2002US-00140474.  
XX  
XX 31-MAR-1997; 97WO-US005230.  
XX 12-JUN-1998; 98WO-US012456.  
XX 14-JUL-1998; 98WO-US014552.  
XX 28-AUG-1998; 98WO-US017888.  
XX 10-SEP-1998; 98WO-US018824.  
XX 14-SEP-1998; 98WO-US019093.  
XX 14-SEP-1998; 98WO-US019094.  
XX 14-SEP-1998; 98WO-US019177.  
XX 16-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
XX 07-OCT-1998; 98WO-US021141.  
XX 29-OCT-1998; 98WO-US022991.  
XX 29-OCT-1998; 98WO-US022992.  
XX 29-OCT-1998; 98WO-US024855.  
XX 01-DEC-1998; 98WO-US025108.  
XX 05-JAN-1999; 99WO-US000106.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99WO-US005190.  
XX 20-APR-1999; 99WO-US008615.  
XX 14-MAY-1999; 99WO-US010733.  
XX 02-JUN-1999; 99WO-US012252.  
XX 01-SEP-1999; 99WO-US020111.  
XX 08-SEP-1999; 99WO-US020594.  
XX 13-SEP-1999; 99WO-US020944.  
XX 15-SEP-1999; 99WO-US021090.  
XX 05-OCT-1999; 99WO-US021547.  
XX 29-NOV-1999; 99WO-US023089.  
XX 30-NOV-1999; 99WO-US028214.  
XX 30-NOV-1999; 99WO-US028313.  
XX 01-DEC-1999; 99WO-US028409.  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028554.  
XX 02-DEC-1999; 99WO-US028555.  
XX

PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 19-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 20-DEC-2000; 2000US-00796498.  
PR 28-FEB-2001; 2001US-0006520.  
PR 01-MAR-2001; 2001WO-US006665.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 05-JUN-2001; 2001WO-US017800.  
PR 14-JUN-2001; 2001US-00874503.  
PR 19-JUN-2001; 2001US-00882636.  
PR 20-JUN-2001; 2001US-00886342.  
PR 21-JUN-2001; 2001WO-US019692.  
PR 22-JUN-2001; 2001US-00887879.  
PR 29-JUN-2001; 2001WO-US020116.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927936.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
XX (GENTH) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z,  
XX WPI; 2003-341980/32.  
XX P-PSDB; ABO17868.



XX New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, acquired immunodeficiency  
PT syndrome (AIDS), or cancer.  
XX  
PS Claim 2; Fig 505; 660pp; English.  
XX  
CC The invention describes an isolated nucleic acid (I) comprising, or which  
CC has 80 % sequence identity to, or the full-length coding sequence of, one  
CC of 275 nucleotide sequences, and which encodes a corresponding  
CC polypeptide selected from 275 amino acid sequences, where all sequences  
CC are given in the specification. The polypeptide encoded by (I) is used to  
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumor necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This sequence encodes a novel human secreted and transmembrane PRO  
CC polypeptide  
XX  
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 5.99e-104 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x ACD24105 (1-1204)

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QY 21 LysThrArgLeuLeuYsGIyAlaIleThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40  
DB 229 AAGAGCGGGCTACTCTGTGGGCGAGCGCTCATCGCCCGGAGTGGCTCTCGAGACAGCC 288  
QY 41 HisCysLeuYsProArgTrpIleValHisLeuGIyHisAsnLeuGlnYsGlnu 60  
DB 289 CACTGCTCAAGCCCGGCTCATAGTTCACCTGGGAGACACAACCTCCGAGAGGAGAG 348  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 349 GGCTGTAGAGAGAGCCGAGACAGCACATGAGTCTCTCCCAACCCCGGCTTCAACAACAGC 408  
QY 81 LeuProAsnYsAspHisArgAsnAspIleMetLeuValYsMetAlaSerProValSer 100  
DB 409 CTCCTCCAAACAAAGACACCCGCAATGATCATGTGTGAAGTGGATGCCAGTCTCC 468  
QY 101 IleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTCGGGCTGTGCGACCCCTCACTCCCTCCACAGCTGTGCATCTGTGCACACAGC 528  
QY 121 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCCTCATTTCCGCTGGGCGAGCATCTCCAGCCCAAGTTACCCCTGCTCACACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnYsCysGluAsnAlaYTrpGlyAsn 160

DB 589 CGATCGGCCCAATCACCATTGAGACACCAAGTGTGAAAGCCTTACCCCGGCAAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlyGIyLysAspSerCysGlnGly 180  
DB 649 ATCAAGACACCATGTGTGTGCGAGCGTGCAGAGAGGGGCGCAAGACTCTGCGCAGGCT 708  
QY 181 AspSerGIyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
DB 709 GACTCCGGGGGCGCTCTGTGTGTACCACTCTTCAAGCATTAATCTCTGGGGCCAG 768  
QY 201 AspProCysAlaIleThrArgLysProGlyValYTrpThrYsValCysLysTrpValAsp 220  
DB 769 GATCGGTGTGCATCAACCCGAAAGCTGTGTCTACAGAAAGCTGCAATAATGTGTGAC 828  
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAACAT 855

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AC ACAA66933;  
XX  
AC 23-JUN-2003 (first entry)  
XX  
DE CDNA encoding human PRO polypeptide #93.  
XX  
KM Human; PRO polypeptide; secreted and transmembrane protein;  
XX anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;  
XX gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003036635-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 28-AUG-2002; 2002US-00230163.  
XX  
PR 25-JUL-2000; 2000US-0220638P.  
XX  
PR 01-JUN-2001; 2001WO-US017800.  
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PR 29-JUN-2001; 2001WO-US021066.  
XX  
PR 09-APR-2002; 2002US-00119480.  
XX  
PA (GENTH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX WPI; 2003-342045/32.  
XX  
DR P-PSDB; AB080831.  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
XX useful for the manufacture of a medicament for diagnosing or treating  
XX tumor.  
XX  
PS Claim 2; Fig 185; 314pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a medicament  
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are  
CC useful in diagnostic assays for PRO, by detecting its expression in  
CC specific cells, tissues or serum, and for affinity purification of PRO  
CC from recombinant cell culture or natural sources. ACAA66841-ACAA66962  
CC represent CDNA sequences encoding the human PRO polypeptides of the  
CC invention. Note: The sequence data for this patent was obtained in  
CC electronic format directly from the USPTO web site at  
CC [seqdata.uspto.gov/psipsideentity.html](http://seqdata.uspto.gov/psipsideentity.html)  
XX  
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	5,99e-104	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x ACA66933 (1-1204)

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QY      21  LyThrArgLeuLeuCySGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
DB      229 AAGAGCGGGCTACTCTGtGGGCGAGCCTCAAGCCCCCAAGTGGCTCTCTGACAGAGCC 288
QY      41  HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysglu 60
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QY      61  GlyCysgluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
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QY      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB      409 CTCCCAACAAGACCAACCCCAATGACATCATGTGTTGAAGATGGCATGGCAGTCTCC 468
QY      101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB      469 ATCACTGGGCTGTGGCAGCCCTCACCTCTCTCAAGCTGTGTCACTGTGGCAGCAGC 528
QY      121 CysLeuLysSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB      529 TGCTCTATTTCGGGCTGGGGCAGCAGCTCCAGCCCCCAATTACGCTGCTCAGACCTTG 588
QY      141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
DB      589 CGATGCCGCCAACAATCACCATCATGAGCACAGAAAGTGAACAGCCCTACCCGGGCAAC 648
QY      161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB      649 ATCAAGAGACCAATGAGTGTGTGCGAGGCTGACAGAGAGGGGCAAGGACTCTGCCAGGGT 708
QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB      709 GACTCCGGGGGCCCTCTGCTGTGAACCAAGTCTCTTCAAGGCATTAATCTCTGGGGCCAG 768
QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB      769 GATCCGTTGCGATCGACCCAGAACCTGTGTCTACACGAAAGTGTGCAATATATGTGGAC 828
QY      221 TrpIleGlnGluThrMetLysAsnAsn 229
DB      829 TGAATCCAGAGAGCATGAAGAACAAT 855

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Search completed: June 23, 2004, 01:43:24

Job time : 463 secs

Thu Jun 24 10:06:29 2004

us-09-856-320a-2\_copy\_54\_282.p2n.rnpb

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: June 23, 2004, 01:35:34 ; Search time 469 Seconds  
(without alignments)  
2236.822 Million cell updates/sec

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Perfect score: 1258  
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Ygapop 10.0 , Ygapext 0.5  
Rgapop 6.0 , Rgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues  
Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database: Published Applications\_NA:

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- 10: /cgn2\_6/ptodata/2/pubna/US09C\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query  
No. Score Match Length DB ID Description

1	1258	100.0	1186	13	US-10-240-425-349	Sequence 349, App
2	1258	100.0	1186	16	US-10-205-823-211	Sequence 211, App
3	1258	100.0	1186	16	US-10-295-027-559	Sequence 559, App
4	1258	100.0	1186	16	US-10-173-999-159	Sequence 159, App
5	1258	100.0	1204	10	US-09-946-374-169	Sequence 169, App
6	1258	100.0	1204	12	US-10-015-395A-169	Sequence 169, App
7	1258	100.0	1204	13	US-10-147-493-505	Sequence 505, App
8	1258	100.0	1204	13	US-10-145-127-505	Sequence 505, App
9	1258	100.0	1204	13	US-10-160-503-505	Sequence 505, App
10	1258	100.0	1204	13	US-10-143-118-505	Sequence 505, App
11	1258	100.0	1204	13	US-10-144-993-505	Sequence 505, App
12	1258	100.0	1204	13	US-10-158-787-505	Sequence 505, App
13	1258	100.0	1204	13	US-10-081-056-207	Sequence 207, App
14	1258	100.0	1204	13	US-10-219-535-185	Sequence 185, App
15	1258	100.0	1204	13	US-10-233-230-185	Sequence 185, App
16	1258	100.0	1204	13	US-10-140-808-505	Sequence 505, App
17	1258	100.0	1204	13	US-10-140-808-505	Sequence 505, App
18	1258	100.0	1204	13	US-10-006-485A-169	Sequence 169, App
19	1258	100.0	1204	13	US-10-013-907A-169	Sequence 169, App
20	1258	100.0	1204	13	US-10-015-499A-169	Sequence 169, App
21	1258	100.0	1204	13	US-10-233-224-185	Sequence 185, App
22	1258	100.0	1204	13	US-10-152-405-505	Sequence 505, App
23	1258	100.0	1204	13	US-10-127-852A-505	Sequence 505, App
24	1258	100.0	1204	13	US-10-127-900A-505	Sequence 505, App
25	1258	100.0	1204	13	US-10-128-685A-505	Sequence 505, App
26	1258	100.0	1204	13	US-10-128-254A-169	Sequence 169, App
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32	1258	100.0	1204	13	US-10-157-798-505	Sequence 505, App
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34	1258	100.0	1204	15	US-10-028-072-505	Sequence 505, App
35	1258	100.0	1204	15	US-10-121-049-505	Sequence 505, App
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42	1258	100.0	1204	15	US-10-137-865-505	Sequence 505, App
43	1258	100.0	1204	15	US-10-140-474-505	Sequence 505, App
44	1258	100.0	1204	15	US-10-142-431-505	Sequence 505, App
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ALIGNMENTS

RESULT 1  
US-10-240-425-349  
Sequence 349, Application US/10240425  
Publication No. US20040033502A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Amanda  
APPLICANT: Boland, Joseph F.  
APPLICANT: Lord, Reginald V.  
APPLICANT: Alvarez, Chris  
APPLICANT: Metzel, Jon C.  
APPLICANT: Scherf, Uwe  
APPLICANT: Vockley, Joseph G.  
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
PTE REFERENCE: 44921-5026  
CURRENT APPLICATION NUMBER: US/10/240,425  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: PCT/US01/09847  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 60/193,446  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 1588  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 349

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; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US2004003502A1 AB012917
US-10-240-425-349

Alignment Scores:
Pred. No.: 4.2e-142 Length: 1186
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-240-425-349 (1-1186)

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DB 185 ATCATCAAGGGGCTTCGAGTGCAGAGCTCATCTCCAGCCCTGCGAGGAGCCCTGTCAG 244
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaIaProArgTyrPheLeuThrAla 40
DB 245 AAGAGCGGCGCTTCTGTGGGGCGACGCTCATCGCCCAAGATGGCTCTCCAGCAGCAGC 304
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGln 60
DB 305 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGCGACCACTCCAGAGAGAGAG 364
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisSerProGlyPheAsnAsnSer 80
DB 365 GGGCTGTGACAGACCCGGGACCACTGATGTCCTCCCGCCCGCTCCCAAGAGAGC 424
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 425 CTCGCCCAAGAGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 484
QY 101 IletThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
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QY 121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisSerThrLeu 140
DB 545 TGCCTCATTTCCGGCTGGGGCGACAGCTCCAGCCCGCCAGTTAGCCCTGCTCCACACCTTG 604
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
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DB 665 ATCAAGACACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 724
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DB 725 GACTCCGGGGGCGCTCTGTGCTGTAAACAGTCTTCAAGGCATTAATCTCTGGGGCAG 784
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220
DB 785 GATCGGTGTGATCACCAGAAAGCTGTGTCTACAGAAAGCTGTCAATATGTGAC 844
QY 221 TrrIleGlnIleThrMetLysAsnAsn 229
DB 845 TGATCCAGAGACGATGAGAAACAT 871

RESULT 2
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; Sequence 211, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.

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; APPLICANT: Ganavara, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamakar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glat, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-211

Alignment Scores:
Pred. No.: 4.2e-142 Length: 1186
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-205-823-211 (1-1186)

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DB 185 ATCATCAAGGGGCTTCGAGTGCAGAGCTCATCTCCAGCCCTGCGAGGAGCCCTGTCAG 244
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaIaProArgTyrPheLeuThrAla 40
DB 245 AAGAGCGGCGCTTCTGTGGGGCGACGCTCATCGCCCAAGATGGCTCTCCAGCAGCAGC 304
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGln 60
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DB 485 ATCACTGGGCTGTGGCGACCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 425 CTCGCCCAAGAGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 484
QY 101 IletThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 485 ATCACTGGGCTGTGGCGACCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisSerThrLeu 140
DB 545 TGCCTCATTTCCGGCTGGGGCGACAGCTCCAGCCCGCCAGTTAGCCCTGCTCCACACCTTG 604
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
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NUMBER OF SEQ ID NOS: 163  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 159  
LENGTH: 1186  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-173-999-159

Alignment Scores:  
Pred. No.: 4,2e-142 Length: 1186  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-10-173-999-159 (1-1186)

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DB 245 AAGAGCGCGCTACTCTGTGGGCGACCGCTCATCCGCCCGATGGCTCTGACGAGCC 304  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
DB 305 CACTGCCCTCAAGCCCGCTACATAGTTCACCTGGGCGACGACCACTCCAGAGAGAG 364  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80  
DB 365 GCGTGTGAGCAGACCGGACGACGACCTGAGTCTTCCCGCCCGCTTCAACAAGC 424  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 425 CTCCCAACAAGACCAAGCAATGACATCGTGGTGAAGATGAGCATGCGCATCTCC 484  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 485 ATCACTGGGCTGTGGGAGCCCTCACTCCCTCAAGCTGTGCACTGGGAGCAGC 544  
QY 121 CysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuAlaGluLeuPheThrLeu 140  
DB 545 TGCCCTATTTCCGGCTGGGCGACGACCTCCAGCCCGCAAGTACCTCCCTCAGCCTTG 604  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
DB 605 CGATCGCCCAATCATCATATGAGGACCAAGAGTGTGAGAGCGCTTACCCCGGAC 664  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
DB 665 ATCAACAGACACCATGTGTGTGCGACGCTGACGAGAGAGGAGGAGCTCTGCGAGGT 724  
QY 181 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTPGlyGln 200  
DB 725 GACTCCGGGAGCCCTCTGGTGTGTGTAACAGTCTCTTAAGCATTAATCTCTGGGAG 784  
QY 201 AspProCysAlaIleThrArgLysProGlyAlaThrIleValCysLysTyrValAsp 220  
DB 785 GATCGGTGTGAGATCACCCGAAAGCTGTGTCTACAGCAAGTCTCAATAATGTGAC 844  
QY 221 TrpIleGlnGlnThrMetLysAsn 229  
DB 845 TGGATCCAGAGACGATGAGACAAAT 871

RESULT 5  
US-09-946-374-169

Sequence 169, Application US/09946374  
Publication No. US20030073129A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Boctstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1  
CURRENT APPLICATION NUMBER: US/09/946,374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
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PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
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PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/098754  
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PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/098808  
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PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/098815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/098816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627

Thu Jun 24 10:06:29 2004

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Page 5

PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
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PRIOR FILING DATE: 1998-09-23  
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PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
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PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30

PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:  
Pred. No.: 4,29e-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-946-374-169 (1-1204)

QY 1 I l e l l e y s g l y h e g i u c y s l y s p r o h i s s e r g i n p r o t r p g i n a l a a l a s u p h e g i u 20  
Db 169 A T C A T C A A G G G T T C G A G T C A A G C C T C A C C C A G C C C T G G A G G C C T G T C G A G 228  
QY 21 L y s T h r a r g l e u e u c y s g l y a l a t m r l e u l l e a l P r o a r g t r p e u e u t h r a l a a l a 40  
Db 229 A A G A C G C G G C T A C T C T G T G G G C A G C G C T A T G C C C C A G A T G G T C C T C G A C A G C C 288  
QY 41 H i s C y s l e u l y s p r o a r g t r y l l e v a l H a s l e u g l y G l n h i s a s n l e u g i n y s g i u j n 60  
Db 289 C A C T G C C T A A G C C C G C T A C A T A G T T C A C C T G G G C A G A C A C C T C C A G A A G A G A G 348  
QY 61 G l y c y s e l u g i n t h r a r g t m r a l a t m r g l u s e r p h e p r o h i s p r o c l y p h e a s n a n s e r 80

DB: 349 GGGTGTGAGCAGACCCGGACAGCAGCTGATGCTTCCCTCCACCCCGGCTTAAACAAGC 408  
QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCGCCAACAAAGACACCGCATGATGCTGGAGATGGCATGGCCAGCTCC 468  
QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCAGCTGGGCTGTGCGACCCCTCACTCTCTCAAGCTGTGATGCTGGAGCAGC 528  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCCCTATTTCGGGTGGGGCAGCAGCTCCAGCCCCCGATTACCCCTCCCAACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleGlnIleGlnLysCysGluAsnAlaTyrProGlyAsn 160  
DB 589 CGATCGGCCAACATACCATCATTTAGACACAGAAAGTGTGAAAGCGCTACCCCGGACAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlyGln 180  
DB 649 ATCACAGACACCATGTGTGTGCGACGCTGCAGAGGGGCGAAGAGACTCTGCGCAGGT 708  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
DB 709 GACTCCGGGGCCCTCTGCTGTGTACAGACTCTCTTCAAGCATTAATCTCTGGGGCAG 768  
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
DB 769 GATCCGTGTGCGATACCCGAAAGCTGTGTCTACACAGAAAGTGTGCAAAATATGTGAC 828  
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAACAT 855

## RESULT 6

US-10-015-395A-169  
Sequence 169, Application US/10015395A  
Publication No. US20040073015A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C57  
CURRENT FILING DATE: 2001-12-12  
Prior application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 169  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-015-395A-169

Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0  
US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-10-015-395A-169 (1-1204)  
QY 1 IleIleLysGlyPheGlnCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGln 20  
DB 169 ATCATCAAGGGGTGAGTGAAGACCTCACTCCAGCCCTGGCAGAGCCCTGTTCAG 228  
QY 21 LysThrArgLeuLeuLysCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40  
DB 229 AAGACGGGCTACTCTGTGGGGCAGACGCTCATCGCCCAAGTGGCTCTTGACACAGCC 288  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGln 60  
DB 289 CACTGCTTAAGCCCGCTCACTACATGTTCACTGGGGCAGACACACTCCAGAGAGAG 348  
QY 61 GlyGlyGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80  
DB 349 GGCTGTGACACAGACCCGACAGACCACTGATCTTCCCTCCCGGCTTCAACAGAC 408  
QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCGCCAACAAAGACACCGCATGATGCTGGAGATGGCATGGCCAGCTTCC 468  
QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCAGCTGGGCTGTGCGACCCCTCACTCTCTCAAGCATTAATCTCTGGGGCAG 528  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCCCTATTTCGGGTGGGGCAGCAGCTCCAGCCCCCGATTACCCCTCCCAACAGC 588  
QY 141 ArgCysAlaAsnIleThrIleIleGlnIleGlnLysCysGluAsnAlaTyrProGlyAsn 160  
DB 589 CGATCGGCCAACATACCATCATTTAGACACAGAAAGTGTGAAAGCGCTACCCCGGACAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlyGln 180  
DB 649 ATCACAGACACCATGTGTGTGCGACGCTGCAGAGGGGCGAAGAGACTCTGCGCAGGT 708  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
DB 709 GACTCCGGGGCCCTCTGCTGTGTACAGACTCTCTTCAAGCATTAATCTCTGGGGCAG 768  
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
DB 769 GATCCGTGTGCGATACCCGAAAGCTGTGTCTACACAGAAAGTGTGCAAAATATGTGAC 828  
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAACAT 855

## RESULT 7

US-10-147-493-505  
Sequence 505, Application US/10147493  
Publication No. US20040029217A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William



APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C345  
; CURRENT APPLICATION NUMBER: US/10/147,493  
; PRIOR APPLICATION: 2002-05-17  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 505  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-147-493-505

Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-147-493-505 (1-1204)

QY 1 IleIleIySGIyPheGluCySlySProHISerGlnProTTPGlnAlaIalaLeuPheGlu 20  
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCTACCTCCAGCCCTTGCGAGGAGCCCTTTCAG 228  
QY 21 LysThrArgLeuLeuCySGIyAlaThrIleuIleAlaProArgTPLeuLeuThrAlaAla 40  
DB 229 AAGAGCGCGTACTCTGTGGGCGAGCGCTCATCGCCCAATGCTGCTGACAGCAGCC 288  
QY 41 HisCysLeuYsProArgTylIleValHisLeuGlyGlnHisAsnLeuGlnGlu 60  
DB 289 CACTGCTCAAGCCCGCTGATAGTTACTGCGGCGAGCAACCTTCGAAAGAGAGG 348  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHISerProGlyPheAsnAsnSer 80  
DB 349 GCGTGTAGCAGACCCCGGACAGCCACTGAGTCTTCCCGCCAGCCCGGCTTCAACAGC 408  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCCCAACAAAGACCCAGCAATGATCATGTGTGAGAGATGGATCGCCAGTCTCC 468  
QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTGGGCTGTGCGACCCCTCACTCTCTCACTGCTGTCTCATCTGCGACAGC 528  
QY 121 CysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCCATATTTCCGGGTGGGCGAGCAGCTCCAGCCCGCTTACCTGCTCAACACTTG 588  
QY 141 ArgCysAlaAsnIleThrIleGlnHisGlnIleCysGlnAsnAlaTyrProGlyAsn 160  
DB 589 CGATGCGCAACATCAATCATTTGAGCAGCAAGAGTGTGAACGCTTACCTCCCGGAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGly 180  
DB 649 ATCAAGACACCATGTGTGTGCCAGCTGCAGAGAGGGGCAAGAGACTCTGCGAGGT 708  
QY 181 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln 200  
DB 709 GACTCGGGGGGCTCTGTGTGTAACCAAGTCTTCAAGGCAATTAATCTCTGGGGCCAG 768  
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
DB 769 GATCGGTGTGATACCCGGAAGGCTGTGTCTACAGAAAGTCTGAAATATGTGAC 828  
QY 221 TTPIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAAACAAT 855  
RESULT 8

US-10-145-127-505  
; Sequence 505, Application US/10145127  
; Publication No. US20040033558A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William

APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C252  
; CURRENT APPLICATION NUMBER: US/10/145,127  
; PRIOR APPLICATION: 2002-05-13  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 505  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-145-127-505

Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-145-127-505 (1-1204)

QY 1 IleIleIySGIyPheGluCySlySProHISerGlnProTTPGlnAlaIalaLeuPheGlu 20  
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCTACCTCCAGCCCTTGCGAGGAGCCCTTTCAG 228  
QY 21 LysThrArgLeuLeuCySGIyAlaThrIleuIleAlaProArgTPLeuLeuThrAlaAla 40  
DB 229 AAGAGCGCGTACTCTGTGGGCGAGCGCTCATCGCCCAATGCTGCTGACAGCAGCC 288  
QY 41 HisCysLeuYsProArgTylIleValHisLeuGlyGlnHisAsnLeuGlnGlu 60  
DB 289 CACTGCTCAAGCCCGCTGATAGTTACTGCGGCGAGCAACCTTCGAAAGAGAGG 348  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHISerProGlyPheAsnAsnSer 80  
DB 349 GCGTGTAGCAGACCCCGGACAGCCACTGAGTCTTCCCGCCAGCCCGGCTTCAACAGC 408  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCCCAACAAAGACCCAGCAATGATCATGTGTGAGAGATGGATCGCCAGTCTCC 468  
QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTGGGCTGTGCGACCCCTCACTCTCTCACTGCTGTCTCATCTGCGACAGC 528  
QY 121 CysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCCATATTTCCGGGTGGGCGAGCAGCTCTTCCCGCCAGCCCGGCTTCAACAGC 588  
QY 141 ArgCysAlaAsnIleThrIleGlnHisGlnIleCysGlnAsnAlaTyrProGlyAsn 160

Db	289	CACGCGCTCAAGCCCGGCTACATAGTTACCTCGGGGGCAGCAACAACCTCCAGAAAGAGAG	348
Qy	61	GLVCSGLUGLInhrTrgThralAmhrgLusePhepcoHsPROGlyPheAsnAsnSer	80
Db	349	GGCGTGAAGAGACCCGGACACCCACTGATCTTCCCAACCCCGCTTCMAAAGAC	408
Qy	81	LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100
Db	409	CTCCCCAACAACCAACCCGCATATGATCATCATGCTGGTGAAGATGGCATGCCAGTCC	468
Qy	101	IleThrTrpAlaValArgProLeuThrLysSerSerArgCysValThrAlaGlyThrSer	120
Db	469	ATACCTGGGGCTGTGGGACCCCTCAACCTCTCTCCACCTGTGTACCTGTGGCAGCAGC	528
Qy	121	CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
Db	529	TGCCTCATTTCCGGCTGGGGCAGACGTCACGCCCTCACTTACCGCTGCTCACAACCTTG	588
Qy	141	ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn	160
Db	589	CGATGGCGCAACATCCATCATTTAGACACCGAAGAGTGTAAGAACGCTACCCGGCAC	648
Qy	161	IleThrAspThrMetValCysAlaSerValGlnGlnGlyValLysAspSerCysGlnGly	180
Db	649	ATACAGACACCCATGTTGTGTCCAGCGGAGGAGGAGGGGAGAGATCTGTGCAGCGT	708
Qy	181	AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	200
Db	709	GACTCGGGGGGCGCTCTGTGTTGTAACCAAGTCTCTTCAAGGCATTATCTCTGGGGCAG	768
Qy	201	AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp	220
Db	769	GATCCGCTGTCCGATCCACCGAAAGCGCTGTCCTACAGAAAGCTCTCAATATGTGAC	828
Qy	221	TrpIleGlnGlyThrMetLysAsnAsn	229
Db	829	TGCATCCAGAGACGATGAGAACAT	855
RESULT 10			
US-10-143-118-505			
; Sequence 505, Application US/10143118			
; Publication No. US2004003835A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Beresini, Maureen			
APPLICANT: Deforge, Laura			
APPLICANT: Destroyers, Luc			
APPLICANT: Filvaroff, Ellen			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Gerritsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurley, Austin L.			
APPLICANT: Sherwood, Steven			
APPLICANT: Smith, Victoria			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Metanabe, Colin K			
APPLICANT: Wood, William			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
FILE REFERENCE: P33081C228			
CURRENT APPLICATION NUMBER: US/10/143,118			
CURRENT FILING DATE: 2002-05-09			
Prior Application removed - See Palm or File Wrapper			
NUMBER OF SEQ ID NOS: 550			
SEQ ID NO 505			
LENGTH: 1204			
TYPE: DNA			
ORGANISM: Homo Sapien			
US-10-143-118-505			

Alignment Scores:

Pred. No.:	4.29e-142	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-856-320A-2\_COPY\_54\_282 (1-229) X US-10-143-118-505 (1-1204)

OY		11	lelleysgllyheglnucylsyprphisserginprotrpglnalalaileuphgln	20
Dd		169	ATATCAAGGGGTTTCGAGTGCACAGCTCATCTCCAGCCTGGCAGGACCCTTGTCAG	228
OY		21	lysThrArgLeuLeuCysgiValatThrIleuileiaProArgTPRpleuLeuThAla	40
Dd		229	AAGCGGGGTACTCTGTGGGGGAGCGCTCATATGCCCGCCCAAGTAGCTCTTCAACAGCAC	288
OY		41	HiscysLeuSerProAgtTrillevalH:sleuglyglnH:sasrleuglnLysglUglu	60
Dd		289	CACGTGCTCAAGCCCCGCTTCAATGTTCACCTGGGGCAGCACAACTCCACAAGAAGAG	348
OY		61	GlycsgluginThArgThAlathrgluserpheProHisPProglyPheasnAsrser	80
Dd		349	GGCTGTAGCAGACCCCGACAGCCATGTAGTCTTCCCACCCCGCTTCAAACACAGC	408
OY		81	LeuProasnLysaspHisarqasnaapilImeleuValLysMetAlaSerProValSer	100
Dd		409	CTCCCCAACAAAGACCCGCAATGAATCATATGCTGTGMAATGGCATTCGCCAGTCTCC	468
OY		101	IleThrTrpAlaValArgrProleuthrLeuSerSerargCysValThralaglyTh-ser	120
Dd		469	ATCACCTGGGTGGGACCCCTCACCCCTCTCTCACGCTGTGTACTGTGGCACAGC	528
OY		121	CysleuIleeserGIYTPRglYserThrserSerProginLeuArxLeuProHisThrLeu	140
Dd		529	TGCTCATATTCGGCTGGGGGACAGCTCCAGCCCCCACTTAAGCTCTCTCACCTTG	588
OY		141	ArgCysAlaasnIleThrIleileglnH:sglnLysCysgluasnalATyP-ProglYasn	160
Dd		589	CGATGGCCCAACATCACATCATATTGAGCACAGAAAGTGTGAGAACGCCATACCCGGCAC	648
OY		161	IleThrspThrMetValCysAlaserValGlngluGlyLysAspSerCysGlngly	180
Dd		649	ATCAACAACACCAATGTGTGTGCCACGTGCAGAGAAAGGGGGAGAGACTCTGCCAGGGT	708
OY		181	AspserGIYglYPRoleuValCysAsnglnSerleuglnglyIleilesertPrpYgln	200
Dd		709	GACTCCGGGGGCGCTCTGTCTTACACAGTCTCTTCAAGGCAATTATCTCGGGGGCAG	768
OY		201	AspProCysAlaIleThrArglySPROGLYValTYThThLysValCysLySTyValASP	220
Dd		769	GATCCGGTGGGATACACCCCAAGCCGTGGTGTCTTACACAAAGTCTGCAAAATATGTGAC	828
OY		221	TriPLEglnGuThrMetLysAsnASN	229
Dd		829	TGATTCACGAGACGATGAAGAACCAT	855
<hr/>				
RESULT 11				
US-10-144-993-505				
Sequence 505, Application US/10144993				
Publication No. US20040038336A1				
GENERAL INFORMATION:				
APPLICANT: Baker, Kevin P.				
APPLICANT: Beresini, Maureen				
APPLICANT: Deforse, Laura				
APPLICANT: Desnoyers, Luc				
APPLICANT: Filvaroff, Ellen				
APPLICANT: Gao, Wei-Qiang				
APPLICANT: Gerritsen, Mary E.				
APPLICANT: Goddard, Audrey J.				
APPLICANT: Godowski, Paul J.				
APPLICANT: Gunney, Austin L.				

## RESULT 11

US-10-144-993-505  
; Sequence 505, Application US/10144993

Publication No. US200400383336A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin H.

**Table 1**

```

1  APPLICANT: Sherwood,Steven
2  APPLICANT: Smith,Victoria
3  APPLICANT: Stewart,Timothy A.
4  APPLICANT: Tumas,Daniel
5  APPLICANT: Watanabe,Colin K
6  APPLICANT: Wood,William
7  APPLICANT: Zhang,Zemin
8  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
9  TITLE OF INVENTION: ACIDS ENCODING THE SAME
10 FILE REFERENCE: P330R1C261
11 CURRENT APPLICATION NUMBER: US/10/144,993
12 CURRENT FILING DATE: 2002-05-13
13 Prior Application removed - See File Wrapper or Palm
14 NUMBER OF SEQ ID NOS: 550
15 SEQ ID NO 505
16 LENGTH: 1204
17 TYPE: DNA
18 ORGANISM: Homo Sapien
19 US-10-144-993-505

```

Alignment Scores:	
Pred. No.:	4,29e-142
Score:	1258.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	13
Length:	120
Matches:	229
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-856-320A-2\_COPY\_54\_282 (1-229) X US-10-144-993-505 (1-1204)

QY	1	IleIleLVsGIPLPhGluLyuSLySproHiseRginPfoTPrGlnAlaAlaLeuPhGlu	20
Db	169	ATCATCAAGGGGTTCAGATGCAAGCTCATCTCCAGCCCTGGCAGGACGCTGTTCAG	228
QY	21	LyeThArgLeuLeuLeuCySGlyAlaThrLeuIleAlaPfoHgtPleLeuThAlaAla	40
Db	229	AAACACCGGCTACTCTGTGGGGCGACGGCTCATCGCCCAATGATCTCTGCACGACGCC	289
QY	41	HicCySLeuLysProHgtIyIleValHisLeuGIyGlnHisAsnLeuGlnLysGIu	60
Db	289	CACGTGCTCAAGCCCGGTACATGATTCACCTGGGGCGACCAACTCCAGAAAGAGAG	348
QY	61	GIYCyGIuGlnThArgThrAlaHndLysPheProHisPProGIyPheAsnSer	80
Db	349	GGCTGTGAGAGACCCGACGACCCACTAGTCTCTCCCAACCCCGGCTTCAACAACAC	408
QY	81	LeuProAsnLysAspHisArgAsnAspIleValLeuValLysMetLysPheValSer	100
Db	409	CTCCCCAACAAGACACCGCAATACATCATGTGCTGGAAGATGGCATCCCGAGTCTCC	468
QY	101	IleThTriAlaValArgProLeuThreusSerArgCyValThrAlaGIYThSer	120
Db	469	ATACCTGGGCTGTGTGACCCCTCAACCTTCTCTACGCTGTGTACATGCTGGGACACAGC	528
QY	121	CysLeuLisSerGIYTPGIYSerThreSerPProGlnLeuAlaGluPProHisThLeu	140
Db	529	TGGCTCATTTCCGGCTGGGGGACAGCTCCAGCCCCCGATACCGCTGCTCACACCTTG	588
QY	141	ArgCyAlaAsnIleThrIleIleGlnHisGlnLysCySGluAsnAlaIyPProGIYAsn	160
Db	589	CGATGGCCCAATCATCCATCATTTAGACACCGAAGTGTGAGAACGGCTATCCCGGCAC	648
QY	161	IleThAspThrMetAlaCysAlaSerValGlnGluGluGIYLysAspSerCyGIuGIY	180
Db	649	ATACACGACACCATGTGTGTGTCCAGCGGACGAGGAGGGGACAAAGACTCTGTCCAGGCT	708
QY	181	AspSerGIYGIYProLeuValCyAsnGlnSerLeuGlnGIYIleIleSerTPGIYGIu	200
Db	709	GACTCCGGGGCCCTGTGTGTGTGAACCAAGTCTCTCAAGCATTAATCTCTCTGGGGCCAG	768
QY	201	AspProCyAlaAlaIleThrArgLysProGIYValIYThrLysValCySLySIYValAsp	220
Db	769	GATCGGTGTGCATACCCGAAAGCTGTGTGTCTACAGAAAGTCTCGAAATATGTGGAC	828

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Qy      221  TtpIleGIngluThrMetLysAsn 229
Db      829  TGAATCCAGAGAGCATGAGAACAT 855

RESULT 12
US-10-158-787-505
/ Sequence 505, Application US/10158787
/ Publication No. US20040039164A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3303R1C449
/ CURRENT FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: US/0158,787
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 505
/ LENGTH: 1204
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-158-787-505

Alignment Scores:
Pred. No.:      4,29e-142      Length:      1204
Score:          1258.00      Matches:      229
Percent Similarity: 100.00%      Mismatches: 0
Best Local Similarity: 100.00%      Indels: 0
Query Match:    100.00%      Gaps: 0
DB: 13

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-158-787-505 (1-1204)

Qy      1  IleIleuysgIyPhegluCyLysProHisserGlnProTrrpGlnAlaAlaLeupheglu 20
Db      169  ATCATCAAGGGGCTTGAAGTCAAGCCTCATCTCCAGGCTCGGAGGAGGAGCCCTGTTGAG 228

Qy      21  LysThrArgLeuLeuCySGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db      229  AAGAGCGGGCTACTCTGTGGGGGAGAGGCTCATGCGCCCAAGATGGCTCCTGACACAGCC 288

Qy      41  HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysglu 60
Db      289  CACTGCTCAAGCCCGCTACATAGTTACCTCGGGGAGCAGCAACCTCCAGAGAGAG 348

Qy      61  GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
Db      349  GGCTGTGACACACCCGAGACCCCTAGTCTCTCCCAAGCTCCCGGCTTCAACACAGC 408

Qy      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db      409  CTCCCAACAAGACACACCGCATATGATCATGCTGTGAAGATGACATCCGCACTTCC 468

Qy      101  IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db      469  ATCACTGGGCTGTGGAGCCCTCACTCTCTCAAGCTGTGTACAGTGGGACAGC 528

Qy      121  CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db      529  TGGCTATTTCGGGCTGGGGGAGAGCTCAAGCCCAAGTTACGCTGCTCAACACTTG 588

Qy      141  ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyProGlyAsn 160
Db      589  CGATGGCCCAATCAATCACTATTAGACACCAAGATGTGAGAACGCTTACCCGAGAC 648

Qy      161  IleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGly 180
Db      649  ATCAAGACACCATGTGTGTGCCAGCGTCAAGAGAGGGGGAAGATCTCCGCGCAGGT 708

Qy      181  AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db      709  GACTCGGGGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768

Qy      201  AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyValAsp 220
Db      769  GATCGGTGTGCATATCAACCGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828

Qy      221  TtpIleGIngluThrMetLysAsn 229
Db      829  TGAATCCAGAGAGCATGAGAACAT 855

RESULT 13
US-10-081-056-207
/ Sequence 207, Application US/10081056
/ Publication No. US20040043927A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Masters, Scot A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Ye, Weilian
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
/ FILE REFERENCE: P3235P1C1
/ CURRENT FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09

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PRIOR FILING DATE: 2001-06-28					
# NUMBER OF SEQ ID NOS: 383					
; SEQ ID NO 207					
; LENGTH: 1204					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
US-10-081-056-207					
Alignment Scores:					
Pred. No.:	4,29e-142	Length:	1204		
Score:	1258.00	Matches:	229		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	13	Gaps:	0		
US-09-856-320A-2_COPY_54_282 (1-229) x US-10-081-056-207 (1-1204)					
QY	1	llellelysglyphgclucyslyseprohisserelncrotrpglnalaaleupheglu	20		
Db	169	ATCATCAAGGGGTTTGAGTGAAGCTTCACCCAGGCCCTGGCAGCGGCCTGTGTGAG	228		
QY	21	lvsthrxleuleucyegjvalathrleullealaproagrtprleuleuthralaia	40		
Db	229	AAGAGCGGCTACTCTGTGGGGCAGCGTCACTCCCCAGATGGCTCTCGACGACGCC	288		
QY	41	HlsCyLeuLysProAlSTyrIleValHlslenglygmhsanleuglnlysgluclu	60		
Db	289	CAGTGCTCAAGCCCCGCTACATAGTTCACTGGGGGAGACAACCTCCGAAGAGAGAG	348		
QY	61	GlyCySgluInThrxgThrAlathglusepheProHisProgiylpheasansSer	80		
Db	349	GGGTGAGACAAACCAGGACACCACTGATCTCTCCCACCCGGCTTCACACACGC	408		
QY	81	LepProAsnLysASPHisArgsnaspillemetleuVallysmetalaserProAlSer	100		
Db	409	CTCCCAACAAAGAACAACCGCAATGATCATCTGCTGGTAAGATGAGCATCGCACATCTCC	468		
QY	101	IleThrTPAlaValArgProleuthreuserearpcysvalThraIaglyThrser	120		
Db	469	ATACCTGGGCGTGGAGACCCCTCACTCTCTCAAGCTGTGCATCTGTGGACACGC	528		
QY	121	CysLeuLisErgJTyrbglyserThrserearProglneuarlgLeuproHisThrlau	140		
Db	529	TGCTCATTTCCGGGCGGGGAGACAGCTCAAGCCCGCATGTAACCTGCTCCACACCTTG	588		
QY	141	ArgCyAlaAsnIleThrIlelleghniSGlnlyscysgluamnalalyrProgiylasn	160		
Db	589	CGATGGCCCAACATCACTCAATCATATTAGAACCAAGGTGTGAAGCGCTTACCCGGGCAAC	648		
QY	161	IleThrAspThrmervalcysalaservalgngluglyglylysaspserCysglnly	180		
Db	649	ATACACGACACCATGTGTGTCTCCAGCTGCAGAGAGGGGGCAAGACTCTCTGCAGGT	708		
QY	181	AspserglycyproleuvalcysanglnserleuglnglyllellesertPrbglyglm	200		
Db	709	GACTCCGGGGGCCCTCTGTGTCTGTACACAGTCTTCAAGGCATTATCTCTGGGGGCGAG	768		
QY	201	AspProCyAlaallethrarglysrprogiyalIyrrThrlvsValCyslysyValasp	220		
Db	769	GATCCTGTGTGCATCAACCCGAAAGCTGTGTCTACAGAAAGTCTGMAATATGTGAC	828		
QY	221	TripIleInglnuThrmellyssansn	229		
Db	829	TGGATCCAAGACGATGAAGAACAAT	855		
RESULT 14					
US-10-219-535-185					
; Sequence 185, Application US/10219535					
; Publication No. US20040044179A1					
; GENERAL INFORMATION:					
; APPLICANT: Baker, Kevin P.					
; APPLICANT: Desnoyers, Luc					

```

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirey, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C60
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 185
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-535-185

Alignment Scores:
Pred. No.: 4,296-142 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-219-535-185 (1-1204)
QY 1 lletlelysglypnehlcyalsyprohisserglnprotglnalaaleupheglu 20
DB 169 ATCATCAAGGGGCTTCGAGTGCAGAGCTCATCCAGCCCTGGAGGAGCCCTGTTCGAG 228
QY 21 lysttharaglsleuycysgllyalaThrlleuilealaproagstplleuThAla 40
DB 229 AAGAGCGGGCTACTCTGTGGGCGAGCGCTCAATCGCCCAATGAGCTCTCCAGCGAGCC 288
QY 41 Hiscysleuysproarglyrilevalhlsleuylglnhlsasleuylnglyslu 60
DB 289 CACTCCCTCAAGCCCGGCTCATATGATTCACCTGGGGGAGCAACCTCCAGAGAGAGAG 348
QY 61 GlycysgluglntharagThAlaThrcgluserpnerohlsprogllypnehsaerSer 80
DB 349 GAGCTGTGAGAGACCCGGAGAGCACTGAGTCTTCCGCCACCCGGGCTTCAACAGAGC 408
QY 81 LeuproasnllyasphlsarGAsnAspillewleuvallysmetalaserProvalser 100
DB 409 CTCGCCAACAAGACCAAGCAATGACATCATCTGCTGGAAGATGCGCATGCCAGTCTCC 468
QY 101 lletthrtplalavalaproleuThrlseuserarGcysvalThralaglyThrSer 120
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DB 469 ATCACTGGGCTTCGACCCCTCACCCCTCTCTCAAGCTGTCTACTGTCGACACAGC 528
QY 121 CysleuileserglytyrpglyserThrSerSerProglInleuArgleuProhlsThrlleu 140
DB 529 TGCCTCATTTCCCGCTGGGGGAGACAGTCGACAGCCCAATTCAGCTCTGCTCAACCTTG 588
QY 141 ArgCysAlasnsllleThrllellelglnhlsleuylnglysluAsnAlaYrProglYan 160
DB 589 GAGTGGCCCAATCCATCCATTCATTGAGCCACAGAGTGTAGAGACCTTACCCGGGAGAC 648
QY 161 lletthAspThrMetValCysAlaserValglnsluylglylsAspserCysglnslly 180
DB 649 ATCAGAGACACCATGAGTGTGTGCAGCGAGAGAGGGGAGAGAGACTCTGCCAGGGGT 708
QY 181 AspSerGlyglyproleuvalCysanglnserleuGlnsllylletleerTrpglygln 200
DB 709 GACTCCGGGGGCTCTGTGTGTACACAGTCTTCAAGGATTAATCTCCGGGGCCAG 768
QY 201 AspProCysAlalleThrArglyspProglYValYrThrlYsValCyslystYrValAsp 220
DB 769 GATCCGTGTGCATACACCGGAAGCCTGAGTGTCTACAGAAAGTCTGCAAAATATGTGAGC 828
QY 221 TplleGlnGlnThrMetlysaAsn 229
DB 829 TCGATCCAGAGAGCATGAAGAAACAT 855

RESULT 15
US-10-232-230-185
Sequence 185, Application US/10232230
Publication No. US2004004180A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirey, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C103
CURRENT FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 185
LENGTH: 1204
TYPE: DNA
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ORGANISM: Homo Sapien  
US-10-232-230-185

US-10-232-230-185

Alignment Scores:

Pred. No.:	4.29e-142	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

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QY	11ellelysglyphegiuCyAlsyPProHsSerGinPOTPrGlnAlaIleuPheGlu 20
Db	169 ATCATCAAGGGGCTTCAGTGCACAGCTCACTCCAGCCCTGGCAGCAGCCCTTTCGAG 228
QY	21 LysThrArgLeuLeuCyGAlaIleuIleuAlaIleuProArgTrpLeuIleuThrAlaIa 40
Db	229 AAGACGCGGCTACTCTGTGGGGGAGAGCGCTCATCGCCCCAGATGAGTCTTCACAGCGAGCC 288
QY	41 HisGlySerLeuysProArgTrpIleValHisIleuGlyGlnHisAsnLeuGlnLysGlu 60
Db	289 CACTGCTCAAGCCCGGCTCATATGTTACCTGGGGCAGCAGACACTTCAGAGAGAGAG 348
QY	61 GlyGluGlnIleuThrArgThrAlaIleuArgIleuSerPheProHisProGlyPheAsnAsnSer 80
Db	349 GCGTGTAGAGAGACCCGGAGCAGCGCATGTAGTCTTCCGCCACCCCGGCTTCACAGACAGC 408
QY	81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValysMetAlaSerProValSer 100
Db	409 CTCCCAACAAAGACCCGCAATGACATCACTGGTGAAGATGGCATCCGCACTCC 468
QY	101 IleThrTrpAlaValArgPProLeuThrLeuSerSerArgCyValThrAlaGlyThrSer 120
Db	469 ATCACTGGGGCTGTGGCAACCCCTCAACCTCTCTCACTGCTGTGATCATGCTGGACACAGC 528
QY	121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db	529 TGCCCTCATTTCCGGCTGGGGCAGACAGTCCAGCCGCCCAATTACGGCTCCCTCAACACCTTG 588
QY	141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCyGluAsnAlaTrpProGlyAsn 160
Db	589 CGATGGCCCAATCATCAATCATTTAGACACACAGAGTGTGAGAAAGCCTACCCCGGCAC 648
QY	161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCyGlnGly 180
Db	649 ATCAACAGACACCAATGTGTGTGTGCACCGTGCAGAGAGGGGGAGAGACACTCTCTGCAGGGT 708
QY	181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db	709 GACTCCGGGGGCCCTCTGTGATCTGTAAACAGTCTCTTCAAGGATTAATCTCTGGGGCCAG 768
QY	201 AspProCysAlaIleuThrArgLysProGlyValIleThrLysValCysLysIleValAsp 220
Db	769 GATCCGCTGGGAGATCAACCGAAAGCCTGGGTGTCTACAGAAAGTCTGCAGAAATATGTGGAC 828
QY	221 TrpIleGlnIleuThrMetLysAsnAsn 229
Db	829 TGGATCCAGAGACGATGAGAAACAAT 855

Search completed: June 23, 2004, 04:01:35  
Job time : 486 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 18:54:57 ; Search time 48 Seconds  
(without alignments)  
1346.871 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IIRGFCKRHPSPWQALFR.....GYTVKCKYVDWIMQETMKKN 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 28213646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PC7\_NEW\_PUB.pep:\*  
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17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1258	100.0	US-09-946-374-170	Sequence 170, App
2	1258	100.0	US-09-933-767-427	Sequence 427, App
3	1258	100.0	US-10-147-493-506	Sequence 506, App
4	1258	100.0	US-10-145-127-506	Sequence 506, App
5	1258	100.0	US-10-160-503-506	Sequence 506, App
6	1258	100.0	US-10-143-118-506	Sequence 506, App
7	1258	100.0	US-10-144-993-506	Sequence 506, App
8	1258	100.0	US-10-158-787-506	Sequence 506, App
9	1258	100.0	US-10-081-056-208	Sequence 208, App
10	1258	100.0	US-10-219-535-186	Sequence 186, App
11	1258	100.0	US-10-232-330-186	Sequence 186, App
12	1258	100.0	US-10-140-024-506	Sequence 506, App
13	1258	100.0	US-10-140-808-506	Sequence 506, App
14	1258	100.0	US-10-004-860-427	Sequence 427, App
15	1258	100.0	US-10-006-485A-170	Sequence 170, App

#### ALIGNMENTS

16	1258	100.0	250	12	US-10-013-907A-170	Sequence 170, App
17	1258	100.0	250	12	US-10-015-499A-170	Sequence 170, App
18	1258	100.0	250	12	US-10-232-324-186	Sequence 186, App
19	1258	100.0	250	12	US-10-013-510A-170	Sequence 170, App
20	1258	100.0	250	12	US-10-152-405-506	Sequence 506, App
21	1258	100.0	250	12	US-10-127-852A-506	Sequence 506, App
22	1258	100.0	250	12	US-10-127-900A-506	Sequence 506, App
23	1258	100.0	250	12	US-10-128-685A-506	Sequence 506, App
24	1258	100.0	250	12	US-10-226-354A-170	Sequence 170, App
25	1258	100.0	250	12	US-10-131-820A-506	Sequence 506, App
26	1258	100.0	250	12	US-10-142-886-506	Sequence 506, App
27	1258	100.0	250	12	US-10-146-128-506	Sequence 506, App
28	1258	100.0	250	12	US-10-146-189-506	Sequence 506, App
29	1258	100.0	250	12	US-10-147-499-506	Sequence 506, App
30	1258	100.0	250	12	US-10-157-798-506	Sequence 506, App
31	1258	100.0	250	12	US-10-305-654-208	Sequence 208, App
32	1258	100.0	250	12	US-10-015-395A-170	Sequence 170, App
33	1258	100.0	250	14	US-10-028-072-506	Sequence 506, App
34	1258	100.0	250	14	US-10-121-049-506	Sequence 506, App
35	1258	100.0	250	14	US-10-123-904-506	Sequence 506, App
36	1258	100.0	250	14	US-10-140-470-506	Sequence 506, App
37	1258	100.0	250	14	US-10-175-746-506	Sequence 506, App
38	1258	100.0	250	14	US-10-176-918-506	Sequence 506, App
39	1258	100.0	250	14	US-10-176-921-506	Sequence 506, App
40	1258	100.0	250	14	US-10-227-884-186	Sequence 186, App
41	1258	100.0	250	14	US-10-137-865-506	Sequence 506, App
42	1258	100.0	250	14	US-10-140-474-506	Sequence 506, App
43	1258	100.0	250	14	US-10-142-431-506	Sequence 506, App
44	1258	100.0	250	14	US-10-143-114-506	Sequence 506, App
45	1258	100.0	250	14	US-10-230-163-186	Sequence 186, App

RESULT 1  
US-09-946-374-170  
Sequence 170, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750



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PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
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PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1258; DB 10; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQPQALFEKTRLLCGATLIAPRMILTAHCKPRITVHLSGHNIQKE 60
DB 22 IIKGFCEKPHSQPQALFEKTRLLCGATLIAPRMILTAHCKPRITVHLSGHNIQKE 81
QY 61 GCEOTRATESFPHPGNNSLPNKDHRNDIMLVMA SPASITVAVRPLTSSRCVTAAGTS 120
DB 82 GCEOTRATESFPHPGNNSLPNKDHRNDIMLVMA SPASITVAVRPLTSSRCVTAAGTS 141
QY 121 CLISGWSSTSPQILRPHTRCANITIEHOKCENAYPGNITDTMVCASVOEGSKDSCQG 180
DB 142 CLISGWSSTSPQILRPHTRCANITIEHOKCENAYPGNITDTMVCASVOEGSKDSCQG 201
QY 181 DSGGPLVNCNLSGIIISMGDPCATIRKPGVYTVCKVYVMIGETMKN 229
DB 202 DSGGPLVNCNLSGIIISMGDPCATIRKPGVYTVCKVYVMIGETMKN 250

RESULT 2
US-09-933-767-427
; Sequence 427; Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007B2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
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PRIOR APPLICATION NUMBER: 60/048,895
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PRIOR APPLICATION NUMBER: 60/068,054
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR FILING DATE: 1997-12-18
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PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
PRIOR FILING DATE: 1998-01-30
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PRIOR FILING DATE: 1998-01-30

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PRIOR APPLICATION NUMBER: 60/073,164  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/085,925  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,921  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,923  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,922  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/092,921  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/094,657  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1245  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO: 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-933-767-427

Query Match 100.0%; Score 1258; DB 10; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKEE 81  
QY 61 GGEOTRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
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QY 121 CLISGWSSTSPQRLPHTLRCAITITIEHOKCENAYPGNITDMVCASVQEGKXSCQG 180  
DB 142 CLISGWSSTSPQRLPHTLRCAITITIEHOKCENAYPGNITDMVCASVQEGKXSCQG 201  
QY 181 DSGGPLVNCNOSLQGIISWGDPICATRKPGVYTVCKYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLQGIISWGDPICATRKPGVYTVCKYVDMIOETMKN 250

RESULT 3  
US-10-147-493-506  
Sequence 506, Application US/10147493  
Publication No. US20040029217A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Mei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C345  
CURRENT APPLICATION NUMBER: US/10/147,493  
CURRENT FILING DATE: 2002-05-17  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506

LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-147-493-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKEE 81  
QY 61 GGEOTRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
DB 82 GGEOTRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSSTSPQRLPHTLRCAITITIEHOKCENAYPGNITDMVCASVQEGKXSCQG 180  
DB 142 CLISGWSSTSPQRLPHTLRCAITITIEHOKCENAYPGNITDMVCASVQEGKXSCQG 201  
QY 181 DSGGPLVNCNOSLQGIISWGDPICATRKPGVYTVCKYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLQGIISWGDPICATRKPGVYTVCKYVDMIOETMKN 250

RESULT 4  
US-10-145-127-506  
Sequence 506, Application US/10145127  
Publication No. US2004003358A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Mei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C345  
CURRENT APPLICATION NUMBER: US/10/145,127  
CURRENT FILING DATE: 2002-05-13  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-145-127-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKEE 81  
QY 61 GGEOTRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
DB 82 GGEOTRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141

QY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVOEGGKDS COG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVOEGGKDS COG 201  
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTRKVCYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTRKVCYVDMIOETMKN 250

## RESULT 5

US-10-160-503-506  
Sequence 506, Application US/10160503  
Publication No. US20040035559A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C446  
CURRENT APPLICATION NUMBER: US/10/160,503  
CURRENT FILING DATE: 2002-05-30  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-160-503-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQWQALFEKTRLLCGATLTAAPRWLLTAHCKRPRIYVHIGQHNLOKEE 60  
DB 22 IIKGFCEKPHSQWQALFEKTRLLCGATLTAAPRWLLTAHCKRPRIYVHIGQHNLOKEE 81  
QY 61 GCEQRTATSPFPHGPNNSLPNKDHRNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSPFPHGPNNSLPNKDHRNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVOEGGKDS COG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVOEGGKDS COG 201  
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTRKVCYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTRKVCYVDMIOETMKN 250

## RESULT 6

US-10-143-118-506  
Sequence 506, Application US/10143118  
Publication No. US20040038335A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C228  
CURRENT APPLICATION NUMBER: US/10/143,118  
CURRENT FILING DATE: 2002-05-09  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-143-118-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQWQALFEKTRLLCGATLTAAPRWLLTAHCKRPRIYVHIGQHNLOKEE 60  
DB 22 IIKGFCEKPHSQWQALFEKTRLLCGATLTAAPRWLLTAHCKRPRIYVHIGQHNLOKEE 81  
QY 61 GCEQRTATSPFPHGPNNSLPNKDHRNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSPFPHGPNNSLPNKDHRNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVOEGGKDS COG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPGNITDTMVCASVOEGGKDS COG 201  
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTRKVCYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTRKVCYVDMIOETMKN 250

## RESULT 7

US-10-144-993-506  
Sequence 506, Application US/10144993  
Publication No. US20040038336A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C261  
CURRENT APPLICATION NUMBER: US/10/144,993

CURRENT FILING DATE: 2002-05-13  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-144-993-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 81  
QY 61 GCEQTRATESPFPFGFNNSLPNKDHRNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQTRATESPFPFGFNNSLPNKDHRNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRPLETTRCANITIIHQKCNAPGNITDTMVCASVOEGKDCOCG 180  
DB 142 CLISGSGTSSPOLRPLETTRCANITIIHQKCNAPGNITDTMVCASVOEGKDCOCG 201  
QY 181 DSGGPLVNCQSLQGIISWGDPICAITRKPGVYTVCKYVDMIOETMKN 229  
DB 202 DSGGPLVNCQSLQGIISWGDPICAITRKPGVYTVCKYVDMIOETMKN 250

RESULT 8  
US-10-158-787-506  
Sequence 506, Application US/10158787  
Publication No. US20040039164A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Desnoyers, Luc  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P33301C49  
CURRENT APPLICATION NUMBER: US/10/158,787  
CURRENT FILING DATE: 2003-04-03  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-158-787-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 81  
QY 61 GCEQTRATESPFPFGFNNSLPNKDHRNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQTRATESPFPFGFNNSLPNKDHRNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRPLETTRCANITIIHQKCNAPGNITDTMVCASVOEGKDCOCG 180  
DB 142 CLISGSGTSSPOLRPLETTRCANITIIHQKCNAPGNITDTMVCASVOEGKDCOCG 201  
QY 181 DSGGPLVNCQSLQGIISWGDPICAITRKPGVYTVCKYVDMIOETMKN 229  
DB 202 DSGGPLVNCQSLQGIISWGDPICAITRKPGVYTVCKYVDMIOETMKN 250

RESULT 9  
US-10-081-056-208

Sequence 208, Application US/10081056  
Publication No. US20040043927A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Geiber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scott A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilian  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS  
FILE REFERENCE: P3335P1C1  
CURRENT APPLICATION NUMBER: US/10/081,056  
CURRENT FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: US 09/643,657  
PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/230,978  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/000,000  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 09/664,610  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/242,922  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 09/709,238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30952  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/767,609  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/796,498  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06666  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/802,706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/808,689  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/828,366  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/866,034  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: PCT/US01/17092  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/870,574  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/17443  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/00000  
PRIOR FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 383  
SEQ ID NO 208  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-081-056-208

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 60  
DB 22 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 81  
QY 61 GGEORRTATESPPHGFNNLSJENKDHNDIMLVMAASPVSTIWAIVPLTSSRCVTAGTS 120  
DB 82 GGEQTRITESPPHGFNNLSJENKDHNDIMLVMAASPVSTIWAIVPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLCANITIIHCKCENAYFGNITDTMVCASVQSGKDSQCG 180  
DB 142 CLISGSGTSSPOLRLPHTLCANITIIHCKCENAYFGNITDTMVCASVQSGKDSQCG 201  
QY 181 DSGGPLVNCQSLQGIISWGDPICATIRPQYTVYCKYVDWIOETMKN 229  
DB 202 DSGGPLVNCQSLQGIISWGDPICATIRPQYTVYCKYVDWIOETMKN 250

RESULT 10  
US-10-219-535-186  
Sequence 186, Application US/10219535  
Publication No. US20040044179A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerilsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Warshaw, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C60  
CURRENT APPLICATION NUMBER: US/10/219,535  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 186  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-219-535-186

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 60  
DB 22 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 81

QY 61 GCEQRTATSEFPHPGNNSLPNKDHNDIMLVMAASVSIITAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSEFPHPGNNSLPNKDHNDIMLVMAASVSIITAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAVPGNITDTMVCASVQEGGKDCSCG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAVPGNITDTMVCASVQEGGKDCSCG 201  
QY 181 DSGGPLVNCNSLQGIISWGDPICATRKPGVYTKVCXYVMIQETMKN 229  
DB 202 DSGGPLVNCNSLQGIISWGDPICATRKPGVYTKVCXYVMIQETMKN 250

RESULT 11  
US-10-232-230-186  
; Sequence 186, Application US/102322230  
; Publication No. US20040044180A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerltsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C103  
CURRENT APPLICATION NUMBER: US/10/232,230  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 186  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-232-230-186

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIGFECKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60  
DB 22 IIGFECKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81  
QY 61 GCEQRTATSEFPHPGNNSLPNKDHNDIMLVMAASVSIITAVRPLTSSRCVTAGTS 120

DB 82 GCEQRTATSEFPHPGNNSLPNKDHNDIMLVMAASVSIITAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAVPGNITDTMVCASVQEGGKDCSCG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAVPGNITDTMVCASVQEGGKDCSCG 201  
QY 181 DSGGPLVNCNSLQGIISWGDPICATRKPGVYTKVCXYVMIQETMKN 229  
DB 202 DSGGPLVNCNSLQGIISWGDPICATRKPGVYTKVCXYVMIQETMKN 250

RESULT 12  
US-10-140-024-506  
; Sequence 506, Application US/10140024  
; Publication No. US20040038424A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530R1C69  
CURRENT APPLICATION NUMBER: US/10/140,024  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-024-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIGFECKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60  
DB 22 IIGFECKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81  
QY 61 GCEQRTATSEFPHPGNNSLPNKDHNDIMLVMAASVSIITAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSEFPHPGNNSLPNKDHNDIMLVMAASVSIITAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAVPGNITDTMVCASVQEGGKDCSCG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAVPGNITDTMVCASVQEGGKDCSCG 201  
QY 181 DSGGPLVNCNSLQGIISWGDPICATRKPGVYTKVCXYVMIQETMKN 229  
DB 202 DSGGPLVNCNSLQGIISWGDPICATRKPGVYTKVCXYVMIQETMKN 250

RESULT 13  
US-10-140-808-506  
; Sequence 506, Application US/10140808  
; Publication No. US20030017563A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.



APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Garitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin J.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C182  
CURRENT FILING DATE: 2002-05-07  
PRIORITY APPLICATION: removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-808-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPWOALFEKTRLLCGATLIAPRWLTAAHCLKRYIVHIGQHNLOKEE 60  
DB 22 IIKGFCKPHSQPWOALFEKTRLLCGATLIAPRWLTAAHCLKRYIVHIGQHNLOKEE 81  
QY 61 GGEQRTATSFPHGFNNSLPNKDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 120  
DB 82 GGEQRTATSFPHGFNNSLPNKDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 141  
QY 121 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGGKDSQCG 180  
DB 142 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGGKDSQCG 201  
QY 181 DSGGPLVNCOSLOGIISWGQPCATRRKPGVYTKVKCYVDWIOETMKN 229  
DB 202 DSGGPLVNCOSLOGIISWGQPCATRRKPGVYTKVKCYVDWIOETMKN 250

RESULT 14  
US-10-004-860-427  
Sequence 427, Application US/10004860  
Publication No. US20030065160A1  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/10/004,860  
CURRENT FILING DATE: 2001-12-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-004-860-427

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPWOALFEKTRLLCGATLIAPRWLTAAHCLKRYIVHIGQHNLOKEE 60  
DB 22 IIKGFCKPHSQPWOALFEKTRLLCGATLIAPRWLTAAHCLKRYIVHIGQHNLOKEE 81  
QY 61 GGEQRTATSFPHGFNNSLPNKDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 120  
DB 82 GGEQRTATSFPHGFNNSLPNKDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 141  
QY 121 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGGKDSQCG 180  
DB 142 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGGKDSQCG 201  
QY 181 DSGGPLVNCOSLOGIISWGQPCATRRKPGVYTKVKCYVDWIOETMKN 229  
DB 202 DSGGPLVNCOSLOGIISWGQPCATRRKPGVYTKVKCYVDWIOETMKN 250

RESULT 15  
US-10-006-485A-170  
Sequence 170, Application US/10006485A  
Publication No. US20030064062A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin J.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1c9  
CURRENT APPLICATION NUMBER: US/10/006,485A  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/095716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
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PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
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PRIOR FILING DATE:	1998-10-07
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PRIOR FILING DATE:	1998-10-20
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PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/105002
PRIOR FILING DATE:	1998-10-20
PRIOR APPLICATION NUMBER:	60/105104
PRIOR FILING DATE:	1998-10-21
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PRIOR FILING DATE:	1998-10-22
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PRIOR FILING DATE:	1998-10-27
PRIOR APPLICATION NUMBER:	60/105881
PRIOR FILING DATE:	1998-10-27
PRIOR APPLICATION NUMBER:	60/105882
PRIOR FILING DATE:	1998-10-27
PRIOR APPLICATION NUMBER:	60/106023
PRIOR FILING DATE:	1998-10-28

Query Match 100.0%; Score 1258; DB 12; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	IIKGFCKPHSQPWQALFEKTRILCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE	60
DB	22	IIKGFCKPHSQPWQALFEKTRILCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE	81
QY	61	GCEQTRTATESPFPNGNNSLPNKDHRNDIMLVKASPVISITAVRPLTLSSRCTAGTS	120
DB	82	GCEQTRTATESPFPNGNNSLPNKDHRNDIMLVKASPVISITAVRPLTLSSRCTAGTS	141
QY	121	CLISGWGSTSSPOLRLPHLTRCANITIIIEHOKCENAYPGNITDTWVCASVQEGKDSCOG	180
DB	142	CLISGWGSTSSPOLRLPHLTRCANITIIIEHOKCENAYPGNITDTWVCASVQEGKDSCOG	201
QY	181	DSGGPLVNCQSLGIIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	229
DB	202	DSGGPLVNCQSLGIIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	250

Search completed: June 22, 2004, 18:58:28  
 Job time : 49 secs

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